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<110> Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.

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- <223> Signal Peptide

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 <222> 18-24, 32-38, 34-40, 35-41, 51-57
 <223> N-Myristoylation Site.

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 <222> 22-26, 50-54, 113-117
 <223> Casein Kinase II Phosphorylation Site.

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 Gly Gln Gly Leu Leu Leu Thr Leu Glu Glu His Ile Ala His Phe
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 35 40 45
 Cys Arg Asp Asp Ser Gly Thr Asp Asp Ser Val Asp Thr Gln Gln
 50 55 60
 Gln Gln Ala Glu Asn Ser Ala Val Pro Thr Ala Asp Thr Arg Ser
 65 70 75
 Gln Pro Arg Asp Pro Val Arg Pro Pro Arg Arg Gly Arg Gly Pro
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 His Glu Pro Arg Arg Lys Lys Gln Asn Val Asp Gly Leu Val Leu
 95 100 105
 Asp Thr Leu Ala Val Ile Arg Thr Leu Val Asp Lys
 110 115

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<220>
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 <222> 4-10, 5-11, 47-53, 170-176, 176-182
 <223> N-Myristoylation Site.

<220>
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 <222> 44-85
 <223> G-protein Coupled Receptors Proteins.

<220>
 <221> misc_feature
 <222> 54-65
 <223> Prokaryotic Membrane Lipoprotein Lipid Attachment Site.

<220>
 <221> misc_feature
 <222> 82-86
 <223> Casein Kinase II Phosphorylation Site.

<220>
 <221> TRANSMEM
 <222> 86-103, 60-75
 <223> Transmembrane Domain

<220>
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 <222> 144-151
 <223> Tyrosine Kinase Phosphorylation Site.

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Leu Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr
 20 25 30
 Phe Val Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr
 35 40 45
 Phe Gly Leu Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile
 50 55 60
 Ser Met Gly Cys Ala Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln
 65 70 75
 His Ala Trp Ala Gln Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr
 80 85 90
 Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr Val Asn Ala Arg Trp
 95 100 105
 Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala Leu Gln Thr Val
 110 115 120
 Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly Ser His Gln
 125 130 135
 Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro Lys Tyr
 140 145 150
 Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser Ser
 155 160 165
 Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala
 170 175 180
 Gly Leu Ala Leu Glu Ile Arg Ser Leu
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<210> 9
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 <212> DNA
 <213> Homo sapiens

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 tacattttta tcaactggatg tgactcgggc tttggaaact tggcagccag 250
 aacttttgat aaaaagggat ttcattgtaat cgctgcctgt ctgactgaat 300
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 cttctggatg tgaccgaccc agagaatgtc aagaggactg cccagtgggt 400

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gaagaaccaa gttggggaga aagggtctctg ggggtctgatc aataatgctg 450
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agagaacctt ttgaagtga cctgttttga ctcactcagt tgacactaaa 550
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tctccagaca tcaaacaaca atatggagaa ggttacattg aaaaaagtct 850
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<210> 10
<211> 319
<212> PRT
<213> Homo sapiens

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<222> 1-17
<223> Signal Peptide

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<220>
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<222> 36-47, 108-113, 166-171,198-203, 207-212
 <223> N-myristoylation Sites.

<220>
 <221> misc feature
 <222> 39-42
 <223> Glycosaminoglycan Attachment Site.

<220>
 <221> TRANSMEM
 <222> 136-152
 <223> Transmembrane Domain

<220>
 <221> misc feature
 <222> 161-163, 187-190 and 253-256
 <223> N-glycosylation Sites.

<400> 10

Met	Leu	Phe	Trp	Val	Leu	Gly	Leu	Leu	Ile	Leu	Cys	Gly	Phe	Leu	1	5	10	15
Trp	Thr	Arg	Lys	Gly	Lys	Leu	Lys	Ile	Glu	Asp	Ile	Thr	Asp	Lys	20	25	30	
Tyr	Ile	Phe	Ile	Thr	Gly	Cys	Asp	Ser	Gly	Phe	Gly	Asn	Leu	Ala	35	40	45	
Ala	Arg	Thr	Phe	Asp	Lys	Lys	Gly	Phe	His	Val	Ile	Ala	Ala	Cys	50	55	60	
Leu	Thr	Glu	Ser	Gly	Ser	Thr	Ala	Leu	Lys	Ala	Glu	Thr	Ser	Glu	65	70	75	
Arg	Leu	Arg	Thr	Val	Leu	Leu	Asp	Val	Thr	Asp	Pro	Glu	Asn	Val	80	85	90	
Lys	Arg	Thr	Ala	Gln	Trp	Val	Lys	Asn	Gln	Val	Gly	Glu	Lys	Gly	95	100	105	
Leu	Trp	Gly	Leu	Ile	Asn	Asn	Ala	Gly	Val	Pro	Gly	Val	Leu	Ala	110	115	120	
Pro	Thr	Asp	Trp	Leu	Thr	Leu	Glu	Asp	Tyr	Arg	Glu	Pro	Ile	Glu	125	130	135	
Val	Asn	Leu	Phe	Gly	Leu	Ile	Ser	Val	Thr	Leu	Asn	Met	Leu	Pro	140	145	150	
Leu	Val	Lys	Lys	Ala	Gln	Gly	Arg	Val	Ile	Asn	Val	Ser	Ser	Val	155	160	165	
Gly	Gly	Arg	Leu	Ala	Ile	Val	Gly	Gly	Gly	Tyr	Thr	Pro	Ser	Lys	170	175	180	
Tyr	Ala	Val	Glu	Gly	Phe	Asn	Asp	Ser	Leu	Arg	Arg	Asp	Met	Lys	185	190	195	

Ala	Phe	Gly	Val	His	Val	Ser	Cys	Ile	Glu	Pro	Gly	Leu	Phe	Lys	
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Thr	Asn	Leu	Ala	Asp	Pro	Val	Lys	Val	Ile	Glu	Lys	Lys	Leu	Ala	
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Ile	Trp	Glu	Gln	Leu	Ser	Pro	Asp	Ile	Lys	Gln	Gln	Tyr	Gly	Glu	
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Gly	Tyr	Ile	Glu	Lys	Ser	Leu	Asp	Lys	Leu	Lys	Gly	Asn	Lys	Ser	
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Tyr	Val	Asn	Met	Asp	Leu	Ser	Pro	Val	Val	Glu	Cys	Met	Asp	His	
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Ala	Leu	Thr	Ser	Leu	Phe	Pro	Lys	Thr	His	Tyr	Ala	Ala	Gly	Lys	
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Asp	Ala	Lys	Ile	Phe	Trp	Ile	Pro	Leu	Ser	His	Met	Pro	Ala	Ala	
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 <212> PRT
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 <222> 21-40 and 84-105
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 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro
 35 40 45
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr
 50 55 60
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp
 65 70 75
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
 80 85 90
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
 95 100 105

Asp His Trp Lys	Ala Leu Ala Phe Arg	Leu Glu Glu Glu Gln Lys	110	115	120
Met Arg Pro Glu	Ile Ala Gly Leu Lys	Pro Ala Asn Pro Pro Val	125	130	135
Leu Pro Ala Pro	Gln Lys Ala Asp Thr	Asp Pro Glu Asn Leu Pro	140	145	150
Glu Ile Ser Ser	Gln Lys Thr Gln Arg	His Ile Gln Arg Gly Pro	155	160	165
Pro His Leu Gln	Ile Arg Pro Pro Ser	Gln Asp Leu Lys Asp Gly	170	175	180
Thr Gln Glu Glu	Ala Thr Lys Arg Gln	Glu Ala Pro Val Asp Pro	185	190	195
Arg Pro Glu Gly	Asp Pro Gln Arg Thr	Val Ile Ser Trp Arg Gly	200	205	210
Ala Val Ile Glu	Pro Glu Gln Gly Thr	Glu Leu Pro Ser Arg Arg	215	220	225
Ala Glu Val Pro	Thr Lys Pro Pro Leu	Pro Pro Ala Arg Thr Gln	230	235	240
Gly Thr Pro Val	His Leu Asn Tyr Arg	Gln Lys Gly Val Ile Asp	245	250	255
Val Phe Leu His	Ala Trp Lys Gly Tyr	Arg Lys Phe Ala Trp Gly	260	265	270
His Asp Glu Leu	Lys Pro Val Ser Arg	Ser Phe Ser Glu Trp Phe	275	280	285
Gly Leu Gly Leu	Thr Leu Ile Asp Ala	Leu Asp Thr Met Trp Ile	290	295	300
Leu Gly Leu Arg	Lys Glu Phe Glu Glu	Ala Arg Lys Trp Val Ser	305	310	315
Lys Lys Leu His	Phe Glu Lys Asp Val	Asp Val Asn Leu Phe Glu	320	325	330
Ser Thr Ile Arg	Ile Leu Gly Gly Leu	Leu Ser Ala Tyr His Leu	335	340	345
Ser Gly Asp Ser	Leu Phe Leu Arg Lys	Ala Glu Asp Phe Gly Asn	350	355	360
Arg Leu Met Pro	Ala Phe Arg Thr Pro	Ser Lys Ile Pro Tyr Ser	365	370	375
Asp Val Asn Ile	Gly Thr Gly Val Ala	His Pro Pro Arg Trp Thr	380	385	390
Ser Asp Ser Thr	Val Ala Glu Val Thr	Ser Ile Gln Leu Glu Phe			

395	400	405
Arg Glu Leu Ser	Arg Leu Thr Gly Asp Lys Lys Phe Gln Glu Ala	
410	415	420
Val Glu Lys Val	Thr Gln His Ile His Gly Leu Ser Gly Lys Lys	
425	430	435
Asp Gly Leu Val	Pro Met Phe Ile Asn Thr His Ser Gly Leu Phe	
440	445	450
Thr His Leu Gly	Val Phe Thr Leu Gly Ala Arg Ala Asp Ser Tyr	
455	460	465
Tyr Glu Tyr Leu	Leu Lys Gln Trp Ile Gln Gly Gly Lys Gln Glu	
470	475	480
Thr Gln Leu Leu	Glu Asp Tyr Val Glu Ala Ile Glu Gly Val Arg	
485	490	495
Thr His Leu Leu	Arg His Ser Glu Pro Ser Lys Leu Thr Phe Val	
500	505	510
Gly Glu Leu Ala	His Gly Arg Phe Ser Ala Lys Met Asp His Leu	
515	520	525
Val Cys Phe Leu	Pro Gly Thr Leu Ala Leu Gly Val Tyr His Gly	
530	535	540
Leu Pro Ala Ser	His Met Glu Leu Ala Gln Glu Leu Met Glu Thr	
545	550	555
Cys Tyr Gln Met	Asn Arg Gln Met Glu Thr Gly Leu Ser Pro Glu	
560	565	570
Ile Val His Phe	Asn Leu Tyr Pro Gln Pro Gly Arg Arg Asp Val	
575	580	585
Glu Val Lys Pro	Ala Asp Arg His Asn Leu Leu Arg Pro Glu Thr	
590	595	600
Val Glu Ser Leu	Phe Tyr Leu Tyr Arg Val Thr Gly Asp Arg Lys	
605	610	615
Tyr Gln Asp Trp	Gly Trp Glu Ile Leu Gln Ser Phe Ser Arg Phe	
620	625	630
Thr Arg Val Pro	Ser Gly Gly Tyr Ser Ser Ile Asn Asn Val Gln	
635	640	645
Asp Pro Gln Lys	Pro Glu Pro Arg Asp Lys Met Glu Ser Phe Phe	
650	655	660
Leu Gly Glu Thr	Leu Lys Tyr Leu Phe Leu Leu Phe Ser Asp Asp	
665	670	675
Pro Asn Leu Leu	Ser Leu Asp Ala Tyr Val Phe Asn Thr Glu Ala	
680	685	690

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tcccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
ggcgccgcgt aggcccgga ggccgggccg gccgggctgc gagcgctgc 50
cccatgcgcc gccgcctctc cgcacgatgt tcccctcgcg gaggaagcg 100
gcgcagctgc cctgggagga cggcaggtcc gggttgctct ccggcggcct 150
ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgctgg 200
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtca ggggacaagg gcaggagacc tcgggccctc cccgtgcctg 300
 ccccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350
 cccaccgcct ggagtgctg gtgcccttcc gogaacgctt cgaggagctc 400
 ctggtcttcg tgccccacat gcgccgcttc ctgagcagga agaagatccg 450
 gcaccacatc tacgtgctca accaggtgga ccacttcagg ttcaaccggg 500
 cagcgctcat caacgtgggc ttcttgaga gcagcaacag cacggactac 550
 attgccatgc acgacgttga cctgtccct ctcaacgagg agctggacta 600
 tggctttcct gaggtgggc ccttccaagt ggccctccccg gagctccacc 650
 ctctctacca ctacaagacc tatgtcggcg gcctcctgct gctctccaag 700
 cagcactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggctgggg 750
 ccgcgaggac gacgagttct accggcgcat taaggagct gggctccagc 800
 ttttccgccc ctcggaatc acaactgggt acaagacatt tcgccacctg 850
 catgaccag cctggcgga gagggaccag aagcgcatcg cagctcaaaa 900
 acaggagcag ttcaaggtgg acaggaggg aggcctgaac actgtgaagt 950
 accatgtggc ttcccgact gccctgtctg tgggcggggc cccctgcact 1000
 gtctcaaca tcatgttga ctgtgacaag accgccacac cctggtgcac 1050
 attcagctga gctggatgga cagtaggaa gcctgtacct acaggccata 1100
 ttgctcaggc tcaggacaag gcctcaggtc gtgggccag ctctgacagg 1150
 atgtggagtg gccaggacca agacagcaag ctacgcaatt gcagccacc 1200
 ggccgccaag gcaggcttg gctgggccag gacacgtggg gtgcctggga 1250
 cgctgottgc catgcacagt gatcagagag aggctgggt gtgtcctgtc 1300
 cgggaccccc cctgccttcc tgctcaccct actctgacct ccttcacgtg 1350
 ccaggcctg tgggtagtgg ggagggtga acaggacaac ctctcatcac 1400
 cctactctga cctccttcac gtgccaggc ctgtgggtag tggggagggg 1450
 tgaacaggac aacctctcat ccccccaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17
 <211> 327
 <212> PRT
 <213> Homo sapiens
 <220>

<221> sig_peptide
 <222> 1-42
 <223> Signal peptide.

<220>
 <221> misc feature
 <222> 19-25,65-71,247-253,285-291,303-310
 <223> N-myristoylation site.

<220>
 <221> misc feature
 <222> 27-31
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
 <221> TRANSMEM
 <222> 29-49
 <223> Transmembrane domain (type II).

<220>
 <221> misc feature
 <222> 154-158
 <223> N-glycosylation site.

<220>
 <221> misc feature
 <222> 226-233
 <223> Tyrosine kinase phosphorylation site.

<400> 17

Met	Phe	Pro	Ser	Arg	Arg	Lys	Ala	Ala	Gln	Leu	Pro	Trp	Glu	Asp	1	5	10	15
Gly	Arg	Ser	Gly	Leu	Leu	Ser	Gly	Gly	Leu	Pro	Arg	Lys	Cys	Ser	20	25	30	
Val	Phe	His	Leu	Phe	Val	Ala	Cys	Leu	Ser	Leu	Gly	Phe	Phe	Ser	35	40	45	
Leu	Leu	Trp	Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Val	Ala	Arg	Ala	50	55	60	
Val	Arg	Gly	Gln	Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg	Ala	Cys	65	70	75	
Pro	Pro	Glu	Pro	Pro	Pro	Glu	His	Trp	Glu	Glu	Asp	Ala	Ser	Trp	80	85	90	
Gly	Pro	His	Arg	Leu	Ala	Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe	95	100	105	
Glu	Glu	Leu	Leu	Val	Phe	Val	Pro	His	Met	Arg	Arg	Phe	Leu	Ser	110	115	120	
Arg	Lys	Lys	Ile	Arg	His	His	Ile	Tyr	Val	Leu	Asn	Gln	Val	Asp	125	130	135	
His	Phe	Arg	Phe	Asn	Arg	Ala	Ala	Leu	Ile	Asn	Val	Gly	Phe	Leu				

140	145	150
Glu Ser Ser Asn Ser Thr Asp Tyr Ile	Ala Met His Asp Val	Asp
155	160	165
Leu Leu Pro Leu Asn Glu Glu Leu Asp	Tyr Gly Phe Pro Glu	Ala
170	175	180
Gly Pro Phe His Val Ala Ser Pro Glu	Leu His Pro Leu Tyr	His
185	190	195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu	Leu Leu Ser Lys Gln	His
200	205	210
Tyr Arg Leu Cys Asn Gly Met Ser Asn	Arg Phe Trp Gly Trp	Gly
215	220	225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg	Ile Lys Gly Ala Gly	Leu
230	235	240
Gln Leu Phe Arg Pro Ser Gly Ile Thr	Thr Gly Tyr Lys Thr	Phe
245	250	255
Arg His Leu His Asp Pro Ala Trp Arg	Lys Arg Asp Gln Lys	Arg
260	265	270
Ile Ala Ala Gln Lys Gln Glu Gln Phe	Lys Val Asp Arg Glu	Gly
275	280	285
Gly Leu Asn Thr Val Lys Tyr His Val	Ala Ser Arg Thr Ala	Leu
290	295	300
Ser Val Gly Gly Ala Pro Cys Thr Val	Leu Asn Ile Met Leu	Asp
305	310	315
Cys Asp Lys Thr Ala Thr Pro Trp Cys	Thr Phe Ser	
320	325	

<210> 18
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 18
 gcgaacgctt cgaggagtcc tgg 23

<210> 19
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-24
 <223> Synthetic construct
 <400> 19
 gcagtgcggg aagccacatg gtac 24

<210> 20
 <211> 46
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-46
 <223> Synthetic construct.

<400> 20
 cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
 <211> 494
 <212> DNA
 <213> Homo sapiens

<400> 21
 caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50
 aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100
 gactggctgg tgcccagaaa gtctcttctg ccaactgacgc ccccatcagg 150
 gattgggcct tctttccccc ttcctttctg tgtctcctgc ctcatcggcc 200
 tgccatgacc tgcagccaag cccagcccg tggggaaggg gagaaagtgg 250
 gggatggcta agaaagctgg gagatagga acagaagagg gtagtgggtg 300
 ggctaggggg gctgccttat ttaaagtggg tgtttatgat tottatacta 350
 atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400
 cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450
 taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22
 <211> 73
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-15
 <223> Signal peptide.

<220>
 <221> misc_feature
 <222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly
1 5 10 15

Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

gggacccatg cggccgtgac ccccggctcc ctagaggccc agcgcagccg 50

cagcggacaa aggagcatgt ccgcgccggg gaaggcccg cctccggccg 100

ccataaggct ccggtcgccg ctggggccgc gccgcgctcc tgcccggccg 150

ggctccgggg cggcccgcta ggccagtgcg ccgccgctcg cccgcaggc 200

cccggcccg agcatggagc caccggagc ccggcggggc cgcgcgcagc 250

cgcgcgtgtt gctgccgctc tcgctgttag cgctgctcgc gctgctggga 300

ggcggcgggc gcggcggcgc cgcggcgctg ccgcgccgct gcaagcacga 350

tgggcgggcc cgaggggctg gcagggcggc gggcgccgcc gagggcaagg 400

tggtgtgcag cagcctgga ctcgcgcagg tctgtcccc agatactctg 450

cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500

gaagaatggc tcattttctg ggttaagtct ccttgaaaga ttggacctcc 550

gaaacaatct tattagtagt atagatccag gtgccttctg gggactgtca 600

tctctaaaaa gattggatct gacaaacaat cgaataggat gtctgaatgc 650

agacatatct cgaggactca ccaatctggt tcggctaaac ctttcgggga 700

atttgttttc ttcattatct caaggaactt ttgattatct tgcgtcatta 750

cggctcttgg aattccagac tgagtatctt ttgtgtgact gtaacatact 800

gtggatgcat cgctgggtaa aggagaagaa catcacggta cgggatacca 850

acatgtgaaa aaattttatt tgacttaaaa gtttatttat ttgttttttt 2350
 gctcctgatt ttaagacaat aagatgtttt catggggcccc taaaagtatc 2400
 atgagccttt ggcaactgcg ctgccaagcc tagtggagaa gtcaaccctg 2450
 agaccaggtg tttaatcaag caagctgtat atcaaaattt ttggcagaaa 2500
 acacaaatat gtcatatatc tttttttaaa aaaagtattt cattgaagca 2550
 agcaaaatga aagcattttt actgatitttt aaaattggtg ctttagatat 2600
 atttgactac actgtattga agcaaataga ggaggcacaa ctccagcacc 2650
 ctaatggaac cacatttttt tcacttagct ttctgtgggc atgtgtaatt 2700
 gtattctctg cggtttttaa tctcacagta ctttattttt gtcttgctcc 2750
 tcaataatat cacaacaat attccagtca ttttaatggc tgcataataa 2800
 ctgatccaac aggtgttagg tgttctggtt tagtgtgagc actcaataaa 2850
 tattgaatga atgaacgaaa aaaaaaaaaa aaa 2883

<210> 24
 <211> 616
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-33
 <223> Signal peptide.

<220>
 <221> TRANSMEM
 <222> 13-40
 <223> Transmembrane domain (type II).

<400> 24
 Met Glu Pro Pro Gly Arg Arg Arg Gly Arg Ala Gln Pro Pro Leu
 1 5 10 15
 Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly
 20 25 30
 Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His
 35 40 45
 Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
 50 55 60
 Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
 65 70 75
 Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
 80 85 90

Asn	Lys	Ile	Ser	Glu	Leu	Lys	Asn	Gly	Ser	Phe	Ser	Gly	Leu	Ser		95	100	105
Leu	Leu	Glu	Arg	Leu	Asp	Leu	Arg	Asn	Asn	Leu	Ile	Ser	Ser	Ile		110	115	120
Asp	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu	Asp		125	130	135
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg		140	145	150
Gly	Leu	Thr	Asn	Leu	Val	Arg	Leu	Asn	Leu	Ser	Gly	Asn	Leu	Phe		155	160	165
Ser	Ser	Leu	Ser	Gln	Gly	Thr	Phe	Asp	Tyr	Leu	Ala	Ser	Leu	Arg		170	175	180
Ser	Leu	Glu	Phe	Gln	Thr	Glu	Tyr	Leu	Leu	Cys	Asp	Cys	Asn	Ile		185	190	195
Leu	Trp	Met	His	Arg	Trp	Val	Lys	Glu	Lys	Asn	Ile	Thr	Val	Arg		200	205	210
Asp	Thr	Arg	Cys	Val	Tyr	Pro	Lys	Ser	Leu	Gln	Ala	Gln	Pro	Val		215	220	225
Thr	Gly	Val	Lys	Gln	Glu	Leu	Leu	Thr	Cys	Asp	Pro	Pro	Leu	Glu		230	235	240
Leu	Pro	Ser	Phe	Tyr	Met	Thr	Pro	Ser	His	Arg	Gln	Val	Val	Phe		245	250	255
Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile	Asp		260	265	270
Gln	Asp	Met	Gln	Val	Leu	Trp	Tyr	Gln	Asp	Gly	Arg	Ile	Val	Glu		275	280	285
Thr	Asp	Glu	Ser	Gln	Gly	Ile	Phe	Val	Glu	Lys	Asn	Met	Ile	His		290	295	300
Asn	Cys	Ser	Leu	Ile	Ala	Ser	Ala	Leu	Thr	Ile	Ser	Asn	Ile	Gln		305	310	315
Ala	Gly	Ser	Thr	Gly	Asn	Trp	Gly	Cys	His	Val	Gln	Thr	Lys	Arg		320	325	330
Gly	Asn	Asn	Thr	Arg	Thr	Val	Asp	Ile	Val	Val	Leu	Glu	Ser	Ser		335	340	345
Ala	Gln	Tyr	Cys	Pro	Pro	Glu	Arg	Val	Val	Asn	Asn	Lys	Gly	Asp		350	355	360
Phe	Arg	Trp	Pro	Arg	Thr	Leu	Ala	Gly	Ile	Thr	Ala	Tyr	Leu	Gln		365	370	375
Cys	Thr	Arg	Asn	Thr	His	Gly	Ser	Gly	Ile	Tyr	Pro	Gly	Asn	Pro				

380	385	390
Gln Asp Glu Arg Lys Ala Trp Arg Arg	Cys Asp Arg Gly Gly Phe	
395	400	405
Trp Ala Asp Asp Asp Tyr Ser Arg Cys	Gln Tyr Ala Asn Asp Val	
410	415	420
Thr Arg Val Leu Tyr Met Phe Asn Gln	Met Pro Leu Asn Leu Thr	
425	430	435
Asn Ala Val Ala Thr Ala Arg Gln Leu	Leu Ala Tyr Thr Val Glu	
440	445	450
Ala Ala Asn Phe Ser Asp Lys Met Asp	Val Ile Phe Val Ala Glu	
455	460	465
Met Ile Glu Lys Phe Gly Arg Phe Thr	Lys Glu Glu Lys Ser Lys	
470	475	480
Glu Leu Gly Asp Val Met Val Asp Ile	Ala Ser Asn Ile Met Leu	
485	490	495
Ala Asp Glu Arg Val Leu Trp Leu Ala	Gln Arg Glu Ala Lys Ala	
500	505	510
Cys Ser Arg Ile Val Gln Cys Leu Gln	Arg Ile Ala Thr Tyr Arg	
515	520	525
Leu Ala Gly Gly Ala His Val Tyr Ser	Thr Tyr Ser Pro Asn Ile	
530	535	540
Ala Leu Glu Ala Tyr Val Ile Lys Ser	Thr Gly Phe Thr Gly Met	
545	550	555
Thr Cys Thr Val Phe Gln Lys Val Ala	Ala Ser Asp Arg Thr Gly	
560	565	570
Leu Ser Asp Tyr Gly Arg Arg Asp Pro	Glu Gly Asn Leu Asp Lys	
575	580	585
Gln Leu Ser Phe Lys Cys Asn Val Ser	Asn Thr Phe Ser Ser Leu	
590	595	600
Ala Leu Lys Val Cys Tyr Ile Leu Gln	Ser Phe Lys Thr Ile Tyr	
605	610	615

Ser

<210> 25

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct

<400> 25

gaggactcac caatctgggt cggc 24

<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

aactggaaag gaaggctgtc tccc 24

<210> 27

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 27

gtaaaggaga agaacatcac ggtacgggat accagggtgtg tttatcctaa 50

<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

gcgtggggat gtctaggagc tcgaagggtg tgctgggcct ctcggtgctg 50
ctgacggcgg ccacagtggc cggcgtacat gtgaagcagc agtgggacca 100
gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcgga 150
aaaaagaaaa cattcgtctt ttgggagAAC agattatctt gactgagcaa 200
cttgaagcag aaagagagaa gatgttattg gcaaaaggat ctcaaaaatc 250
atgacttgaa tgtgaaatat ctgttgga gacaacacga gtttgtgtgt 300
gtgtgttgat ggagagtagc ttagtagtat cttcatcttt ttttttggtc 350
actgtccttt taaacttgat caaataaagg acagtgggtc atataagtta 400
ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450
tttggaagag tctgtctggg tgatcctggt agaagcccca ttagggtcac 500
tgtccagtgc ttaggggtgt tactgagaag cactgccgag cttgtgagaa 550

ggaagggatg gatagtagca tccacctgag tagtctgac agtcggcatg 600
 atgacgaagc cagcagaaca tcgacctcag aaggactgga ggaaggtgaa 650
 gtggagggag agacgctcct gatcgtcgaa tcc 683

<210> 29
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-21
 <223> Signal peptide.

<400> 29
 Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu
 1 5 10 15
 Thr Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp
 20 25 30
 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
 35 40 45
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
 50 55 60
 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
 65 70 75
 Lys Gly Ser Gln Lys Ser
 80

<210> 30
 <211> 2128
 <212> DNA
 <213> Homo sapiens

<400> 30
 ctgtcgtctt tgcttcagcc gcagtcgcca ctggctgcct gagtgctct 50
 tacagcctgt tccaagtgtg gcttaatccg tctccaccac cagatctttc 100
 tccgtggatt cctctgctaa gaccgctgcc atgccagtga cggttaaccg 150
 caccaccatc acaaccacca cgacgtcatc ttcggggcctg ggggtcccca 200
 tgatcgtggg gtcccctcgg gccctgacac agcccctggg tctccttcgc 250
 ctgctgcagc tgggtgtctac ctgctgggcc ttctcgtctg tggctagcgt 300
 gggcgccctgg acgggggtcca tgggcaactg gtccatgttc acctggtgct 350
 tctgcttctc cgtgaccctg atcatcctca tcgtggagct gtgcgggctc 400
 caggcccgtc tccccctgtc ttggcgcaac ttccccatca ccttcgctg 450

attaaaaaac atatatatat atatatttgg aggtcagtaa tttccaatgg 1950
 gcgggaggca ttaagcaccg accctgggtc cctaggcccc gcctggcact 2000
 cagccttgcc agagattggc tccagaattt ttgccaggct tacagaacac 2050
 ccactgccta gaggccatct taaaggaagc aggggctgga tgcctttcat 2100
 cccaactatt ctctgtggta tgaaaaag 2128

<210> 31

<211> 322

<212> PRT

<213> Homo sapiens

<400> 31

Met	Pro	Val	Thr	Val	Thr	Arg	Thr	Thr	Ile	Thr	Thr	Thr	Thr	Thr	1	5	10	15
Ser	Ser	Ser	Gly	Leu	Gly	Ser	Pro	Met	Ile	Val	Gly	Ser	Pro	Arg	20	25	30	
Ala	Leu	Thr	Gln	Pro	Leu	Gly	Leu	Leu	Arg	Leu	Leu	Gln	Leu	Val	35	40	45	
Ser	Thr	Cys	Val	Ala	Phe	Ser	Leu	Val	Ala	Ser	Val	Gly	Ala	Trp	50	55	60	
Thr	Gly	Ser	Met	Gly	Asn	Trp	Ser	Met	Phe	Thr	Trp	Cys	Phe	Cys	65	70	75	
Phe	Ser	Val	Thr	Leu	Ile	Ile	Leu	Ile	Val	Glu	Leu	Cys	Gly	Leu	80	85	90	
Gln	Ala	Arg	Phe	Pro	Leu	Ser	Trp	Arg	Asn	Phe	Pro	Ile	Thr	Phe	95	100	105	
Ala	Cys	Tyr	Ala	Ala	Leu	Phe	Cys	Leu	Ser	Ala	Ser	Ile	Ile	Tyr	110	115	120	
Pro	Thr	Thr	Tyr	Val	Gln	Phe	Leu	Ser	His	Gly	Arg	Ser	Arg	Asp	125	130	135	
His	Ala	Ile	Ala	Ala	Thr	Phe	Phe	Ser	Cys	Ile	Ala	Cys	Val	Ala	140	145	150	
Tyr	Ala	Thr	Glu	Val	Ala	Trp	Thr	Arg	Ala	Arg	Pro	Gly	Glu	Ile	155	160	165	
Thr	Gly	Tyr	Met	Ala	Thr	Val	Pro	Gly	Leu	Leu	Lys	Val	Leu	Glu	170	175	180	
Thr	Phe	Val	Ala	Cys	Ile	Ile	Phe	Ala	Phe	Ile	Ser	Asp	Pro	Asn	185	190	195	
Leu	Tyr	Gln	His	Gln	Pro	Ala	Leu	Glu	Trp	Cys	Val	Ala	Val	Tyr	200	205	210	

Ala	Ile	Cys	Phe	Ile	Leu	Ala	Ala	Ile	Ala	Ile	Leu	Leu	Asn	Leu	
				215					220					225	
Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	Pro	Phe	Pro	Ser	Phe	Leu	
				230					235					240	
Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	Tyr	Ala	Thr	Ala	Leu	
				245					250					255	
Val	Leu	Trp	Pro	Leu	Tyr	Gln	Phe	Asp	Glu	Lys	Tyr	Gly	Gly	Gln	
				260					265					270	
Pro	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	His	Ala	Tyr	
				275					280					285	
Tyr	Val	Cys	Ala	Trp	Asp	Arg	Arg	Leu	Ala	Val	Ala	Ile	Leu	Thr	
				290					295					300	
Ala	Ile	Asn	Leu	Leu	Ala	Tyr	Val	Ala	Asp	Leu	Val	His	Ser	Ala	
				305					310					315	
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<211> 3680

<212> DNA

<213> Homo sapiens

<400> 32

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<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

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Ser Leu Ala Gln Val Asn Leu Ser Pro Phe Ser His Pro Lys Val
35 40 45

His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu
50 55 60

Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu
65 70 75

Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro
80 85 90

Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys
95 100 105

Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala
110 115 120

Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg
125 130 135

Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys
140 145 150

Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp
155 160 165

Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala
170 175 180

Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly
185 190 195

His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu
200 205 210

Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser
215 220 225

Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu
230 235 240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro
245 250 255

Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala
260 265 270

Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser
275 280 285

Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu
290 295 300

Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser
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Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala
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Glu Pro Glu Glu Gln
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<210> 34
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<212> DNA
<213> Artificial

<220>
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<222> 1-25
<223> Synthetic construct

<400> 34
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<210> 35
<211> 50
<212> DNA
<213> Artificial

<220>
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<223> Synthetic construct.

<400> 35
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<210> 36
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<220>
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<222> 1-25
<223> Synthetic construct.

<400> 36

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<210> 37

<211> 23

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<222> 1-23

<223> Synthetic construct.

<400> 37

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<210> 38

<211> 39

<212> DNA

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<222> 1-39

<223> Synthetic construct.

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<221> Artificial sequence

<222> 1-22

<223> Synthetic construct.

<400> 39

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<210> 40

<211> 2084

<212> DNA

<213> Homo sapiens

<400> 40

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<210> 41

<211> 334

<212> PRT

<213> Homo sapiens

<400> 41

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				20					25					30
Thr	Thr	Gln	Asn	Ile	Ala	Glu	Val	Phe	Lys	Thr	Met	Glu	Asn	Lys
				35					40					45
Pro	Ile	Ser	Leu	Glu	Ser	Glu	Ala	Asn	Leu	Asn	Ser	Asp	Lys	Glu
				50					55					60
Asn	Ile	Thr	Thr	Ser	Asn	Leu	Lys	Ala	Ser	His	Ser	Pro	Pro	Leu
				65					70					75
Asn	Leu	Pro	Asn	Asn	Ser	His	Gly	Ile	Thr	Asp	Phe	Ser	Ser	Asn
				80					85					90
Ser	Ser	Ala	Glu	His	Ser	Leu	Gly	Ser	Leu	Lys	Pro	Thr	Ser	Thr
				95					100					105
Ile	Ser	Thr	Ser	Pro	Pro	Leu	Ile	His	Ser	Phe	Val	Ser	Lys	Val
				110					115					120
Pro	Trp	Asn	Ala	Pro	Ile	Ala	Asp	Glu	Asp	Leu	Leu	Pro	Ile	Ser
				125					130					135
Ala	His	Pro	Asn	Ala	Thr	Pro	Ala	Leu	Ser	Ser	Glu	Asn	Phe	Thr
				140					145					150
Trp	Ser	Leu	Val	Asn	Asp	Thr	Val	Lys	Thr	Pro	Asp	Asn	Ser	Ser
				155					160					165
Ile	Thr	Val	Ser	Ile	Leu	Ser	Ser	Glu	Pro	Thr	Ser	Pro	Ser	Val
				170					175					180
Thr	Pro	Leu	Ile	Val	Glu	Pro	Ser	Gly	Trp	Leu	Thr	Thr	Asn	Ser
				185					190					195

Asp	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
				200					205					210
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
				215					220					225
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
				230					235					240
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
				245					250					255
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
				260					265					270
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
				275					280					285
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
				290					295					300
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
				305					310					315
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu
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Arg	Thr	Ser	Val											

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 <212> DNA
 <213> Homo sapiens

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<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

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Glu	Ala	Arg	Gln	Asp	Val	Glu	Ala	Leu	Leu	Ser	Arg	Thr	Val	Arg
			20					25						30

Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu
			35					40						45

Lys	Glu	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
Ser Phe Ile Leu Ala Gly Leu Ile Val	Gly Gly Ala Cys Ile Tyr	
65	70	75
Lys Tyr Phe Met Pro Lys Ser Thr Ile	Tyr Arg Gly Glu Met Cys	
80	85	90
Phe Phe Asp Ser Glu Asp Pro Ala Asn	Ser Leu Arg Gly Gly Glu	
95	100	105
Pro Asn Phe Leu Pro Val Thr Glu Glu	Ala Asp Ile Arg Glu Asp	
110	115	120
Asp Asn Ile Ala Ile Ile Asp Val Pro	Val Pro Ser Phe Ser Asp	
125	130	135
Ser Asp Pro Ala Ala Ile Ile His Asp	Phe Glu Lys Gly Met Thr	
140	145	150
Ala Tyr Leu Asp Leu Leu Leu Gly Asn	Cys Tyr Leu Met Pro Leu	
155	160	165
Asn Thr Ser Ile Val Met Pro Pro Lys	Asn Leu Val Glu Leu Phe	
170	175	180
Gly Lys Leu Ala Ser Gly Arg Tyr Leu	Pro Gln Thr Tyr Val Val	
185	190	195
Arg Glu Asp Leu Val Ala Val Glu Glu	Ile Arg Asp Val Ser Asn	
200	205	210
Leu Gly Ile Phe Ile Tyr Gln Leu Cys	Asn Asn Arg Lys Ser Phe	
215	220	225
Arg Leu Arg Arg Arg Asp Leu Leu Leu	Gly Phe Asn Lys Arg Ala	
230	235	240
Ile Asp Lys Cys Trp Lys Ile Arg His	Phe Pro Asn Glu Phe Ile	
245	250	255
Val Glu Thr Lys Ile Cys Gln Glu		
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<210> 44

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-24

<223> Synthetic construct.

<400> 44

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<210> 45

<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-20
<223> Synthetic construct.

<400> 45
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<210> 46
<211> 26
<212> DNA
<213> Artificial

<220>
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<222> 1-26
<223> Synthetic construct.

<400> 46
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<210> 47
<211> 28
<212> DNA
<213> Artificial

<220>
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<222> 1-28
<223> Synthetic construct.

<400> 47
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<210> 48
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 48
cacgattccc tccacagcaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

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 ggcaggaggt cctctcccc atccctccat ctggggctcc cccaacctct 1850
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 attccggcct gaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1950
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<210> 50

<211> 283

<212> PRT

<213> Homo sapiens

<400> 50

Met	Val	Ser	Ala	Ala	Ala	Pro	Ser	Leu	Leu	Ile	Leu	Leu	Leu	Leu	
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Leu	Leu	Gly	Ser	Val	Pro	Ala	Thr	Asp	Ala	Arg	Ser	Val	Pro	Leu	
				20					25					30	
Lys	Ala	Thr	Phe	Leu	Glu	Asp	Val	Ala	Gly	Ser	Gly	Glu	Ala	Glu	
				35					40					45	
Gly	Ser	Ser	Ala	Ser	Ser	Pro	Ser	Leu	Pro	Pro	Pro	Trp	Thr	Pro	
				50					55					60	
Ala	Leu	Ser	Pro	Thr	Ser	Met	Gly	Pro	Gln	Pro	Thr	Thr	Leu	Gly	
				65					70					75	
Gly	Pro	Ser	Pro	Pro	Thr	Asn	Phe	Leu	Asp	Gly	Ile	Val	Asp	Phe	
				80					85					90	
Phe	Arg	Gln	Tyr	Val	Met	Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala	
				95					100					105	
Phe	Leu	Leu	Met	Phe	Ile	Val	Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln	
				110					115					120	
Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr	Pro	Ser	Ser	Phe	Pro	Lys	Lys	
				125					130					135	
Lys	Tyr	Val	Asp	Gln	Ser	Asp	Arg	Ala	Gly	Gly	Pro	Arg	Ala	Phe	
				140					145					150	
Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser	Arg	Pro	Glu	Glu	Ala	
				155					160					165	

Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr	170	175	180
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp	185	190	195
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys	200	205	210
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro	215	220	225
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu	230	235	240
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly	245	250	255
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro	260	265	270
Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val			275	280	

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 <211> 1734
 <212> DNA
 <213> Homo sapiens

<400> 51
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 52

<211> 440

<212> PRT

<213> Homo sapiens

<400> 52

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Leu	Gly	Ser	Gly	Glu	Ala	Gly	Pro	Leu	Gln	Ser	Gly	Glu	Glu	Ser
				20					25					30

Thr	Gly	Thr	Asn	Ile	Gly	Glu	Ala	Leu	Gly	His	Gly	Leu	Gly	Asp
				35					40					45

Ala	Leu	Ser	Glu	Gly	Val	Gly	Lys	Ala	Ile	Gly	Lys	Glu	Ala	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr		
65	70	75
Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly		
80	85	90
Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala		
95	100	105
Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val		
110	115	120
Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val		
125	130	135
Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile		
140	145	150
Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro		
155	160	165
Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser		
170	175	180
Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln		
185	190	195
Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly		
200	205	210
Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln		
215	220	225
Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly		
230	235	240
Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser		
245	250	255
Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly		
260	265	270
Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser		
275	280	285
Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Asn Ser Gly Gly Ser		
290	295	300
Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly		
305	310	315
Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly Asn Gly His		
320	325	330
Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly		
335	340	345

Glu Ser Gly Ile	Gln Gly Phe Arg Gly	Gln Gly Val Ser Ser Asn
350	355	360
Met Arg Glu Ile	Ser Lys Glu Gly Asn Arg	Leu Leu Gly Gly Ser
365	370	375
Gly Asp Asn Tyr	Arg Gly Gln Gly Ser Ser	Trp Gly Ser Gly Gly
380	385	390
Gly Asp Ala Val	Gly Gly Val Asn Thr Val	Asn Ser Glu Thr Ser
395	400	405
Pro Gly Met Phe	Asn Phe Asp Thr Phe Trp	Lys Asn Phe Lys Ser
410	415	420
Lys Leu Gly Phe	Ile Asn Trp Asp Ala Ile	Asn Lys Asp Gln Arg
425	430	435
Ser Ser Arg Ile	Pro	
440		

<210> 53
 <211> 3580
 <212> DNA
 <213> Homo sapiens

<400> 53
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 ctctcctgct gcgcctgcac cggagcttgg tgttgctgca ggagagttag 200
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<400> 54

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Leu	Phe	Gln	Ile	Pro	Thr	Val	Pro	Glu	Asp	Leu	Phe	Phe	Leu	Glu
			20						25					30
Glu	Gly	Pro	Ser	Tyr	Ala	Phe	Glu	Val	Asp	Thr	Val	Ala	Pro	Glu
			35						40					45
His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
			50						55					60
Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
			65						70					75
Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
			80						85					90
Ile	Thr	Pro	Thr	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln
			95						100					105
Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His
			110						115					120
Asn	Gln	Pro	Pro	Ser	Leu	Arg	Arg	Thr	Val	Glu	Phe	Val	Ala	Glu
			125						130					135
Arg	Ile	Gly	Ser	Asn	Cys	Val	Lys	His	Ile	Lys	Ala	Thr	Leu	Val
			140						145					150
Ala	Asp	Leu	Val	Arg	Gln	Ala	Glu	Ser	Leu	Leu	Gln	Glu	Gln	Leu
			155						160					165
Val	Thr	Gln	Gly	Glu	Glu	Gly	Gly	Asp	Pro	Ala	Gln	Leu	Leu	Glu
			170						175					180
Ile	Leu	Cys	Ser	Gln	Leu	Cys	Pro	His	Gly	Ala	Gln	Ala	Leu	Ala
			185						190					195
Leu	Gly	Arg	Glu	Phe	Cys	Gln	Arg	Lys	Ser	Pro	Gly	Ala	Val	Arg
			200						205					210
Ala	Leu	Leu	Pro	Glu	Glu	Thr	Pro	Ala	Ala	Val	Leu	Ser	Ser	Ala
			215						220					225
Glu	Asn	Ile	Ala	Val	Gly	Leu	Ala	Thr	Glu	Lys	Ala	Cys	Ala	Trp
			230						235					240
Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala
			245						250					255
Ala	Val	Ser	Arg	Thr	Leu	Arg	Ala	Gln	Gly	Pro	Glu	Pro	Ala	Ala
			260						265					270
Arg	Gly	Glu	Arg	Arg	Gly	Cys	Ser	Arg	Ala					
			275						280					

<210> 55
<211> 2401
<212> DNA
<213> Homo sapiens

<400> 55
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a 2401

<210> 56

<211> 299

<212> PRT

<213> Homo sapiens

<400> 56

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Phe	Ala	Leu	Ile	Thr	Ile	Leu	Ile	Leu	Tyr	Ser	Ser	Asn	Ser	Ala
			20						25					30

Asn	Glu	Val	Phe	His	Tyr	Gly	Ser	Leu	Arg	Gly	Arg	Ser	Arg	Arg	
				35					40					45	
Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro	
				50					55					60	
Ile	Leu	Gly	Asn	Lys	Thr	Leu	Pro	Ser	Arg	Cys	His	Gln	Cys	Val	
				65					70					75	
Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro	
				80					85					90	
Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro	
				95					100					105	
Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg	
				110					115					120	
Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln	
				125					130					135	
Glu	Phe	Val	Asn	Arg	Thr	Pro	Glu	Thr	Val	Phe	Ile	Phe	Trp	Gly	
				140					145					150	
Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val	
				155					160					165	
Ile	Gln	Arg	Ala	Gly	Leu	Val	Phe	Pro	Asn	Met	Glu	Ala	Tyr	Ala	
				170					175					180	
Val	Ser	Pro	Gly	Arg	Met	Arg	Gln	Phe	Asp	Asp	Leu	Phe	Arg	Gly	
				185					190					195	
Glu	Thr	Gly	Lys	Asp	Arg	Glu	Lys	Ser	His	Ser	Trp	Leu	Ser	Thr	
				200					205					210	
Gly	Trp	Phe	Thr	Met	Val	Ile	Ala	Val	Glu	Leu	Cys	Asp	His	Val	
				215					220					225	
His	Val	Tyr	Gly	Met	Val	Pro	Pro	Asn	Tyr	Cys	Ser	Gln	Arg	Pro	
				230					235					240	
Arg	Leu	Gln	Arg	Met	Pro	Tyr	His	Tyr	Tyr	Glu	Pro	Lys	Gly	Pro	
				245					250					255	
Asp	Glu	Cys	Val	Thr	Tyr	Ile	Gln	Asn	Glu	His	Ser	Arg	Lys	Gly	
				260					265					270	
Asn	His	His	Arg	Phe	Ile	Thr	Glu	Lys	Arg	Val	Phe	Ser	Ser	Trp	
				275					280					285	
Ala	Gln	Leu	Tyr	Gly	Ile	Thr	Phe	Ser	His	Pro	Ser	Trp	Thr		
				290					295						

<210> 57
 <211> 4277
 <212> DNA
 <213> Homo sapiens

<400> 57

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<210> 58
<211> 1115

<212> PRT

<213> Homo sapiens

<400> 58

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Val	Thr	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Thr	Ala	Gly	Cys	Phe	Ala	
				20					25					30	
Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr	
				35					40					45	
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu	
				50					55					60	
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu	
				65					70					75	
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr	
				80					85					90	
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	
				95					100					105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	
				110					115					120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	
				125					130					135	
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	
				140					145					150	
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	
				155					160					165	
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	
				170					175					180	
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu	
				185					190					195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	
				200					205					210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	
				215					220					225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	
				230					235					240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	
				245					250					255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	
				260					265					270	

Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile	860	865	870
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln	875	880	885
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro	890	895	900
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His	905	910	915
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala	920	925	930
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala	935	940	945
Val	Gly	Tyr	Pro	Gly	Met	Lys	Pro	Gln	Gln	His	Cys	Pro	Gly	Glu	950	955	960
Leu	Gln	Gln	Gln	Ser	Asp	Thr	Ser	Ser	Leu	Leu	Arg	Gln	Thr	His	965	970	975
Leu	Gly	Asn	Gly	Tyr	Asp	Pro	Gln	Ser	His	Gln	Ile	Thr	Arg	Gly	980	985	990
Pro	Lys	Ser	Ser	Pro	Asp	Glu	Gly	Ser	Phe	Leu	Tyr	Thr	Leu	Pro	995	1000	1005
Asp	Asp	Ser	Thr	His	Gln	Leu	Leu	Gln	Pro	His	His	Asp	Cys	Cys	1010	1015	1020
Gln	Arg	Gln	Glu	Gln	Pro	Ala	Ala	Val	Gly	Gln	Ser	Gly	Val	Arg	1025	1030	1035
Arg	Ala	Pro	Asp	Ser	Pro	Val	Leu	Glu	Ala	Val	Trp	Asp	Pro	Pro	1040	1045	1050
Phe	His	Ser	Gly	Pro	Pro	Cys	Cys	Leu	Gly	Leu	Val	Pro	Val	Glu	1055	1060	1065
Glu	Val	Asp	Ser	Pro	Asp	Ser	Cys	Gln	Val	Ser	Gly	Gly	Asp	Trp	1070	1075	1080
Cys	Pro	Gln	His	Pro	Val	Gly	Ala	Tyr	Val	Gly	Gln	Glu	Pro	Gly	1085	1090	1095
Met	Gln	Leu	Ser	Pro	Gly	Pro	Leu	Val	Arg	Val	Ser	Phe	Glu	Thr	1100	1105	1110
Pro	Pro	Leu	Thr	Ile											1115		

<210> 59

<211> 25

<212> DNA

<213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 59
 gggaaacaca gcagtcattg cctgc 25

<210> 60
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 60
 gcacacgtag cctgtcgctg gaggc 24

<210> 61
 <211> 42
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-42
 <223> Synthetic construct.

<400> 61
 cccccaaaag cccaggtccg gtacagcgctc aaacaagagt gg 42

<210> 62
 <211> 1661
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 678
 <223> unknown base

<400> 62
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 cacggggccgc gaggggtccc gcgcgctcag ccggcggtat ctgcggcgctc 150
 tgctgctcct gctactgctg ctgctgctgc ggcagcccgt aacccgcgcg 200
 gagaccacgc cgggcgcccc cagagccctc tccacgctgg gctccccag 250
 cctcttcacc acgcccgggtg tcccagcgc cctcactacc ccaggcctca 300
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ctgatgcgga gtttcccact cgtggacggc cacaatgacc tgccccaggt 400
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 cacatggaaa a 1661

<210> 63
 <211> 487
 <212> PRT
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 196, 386
 <223> unknown amino acid

<400> 63

Met	Gln	Pro	Thr	Gly	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg	1	5	10	15
Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	20	25	30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	35	40	45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	50	55	60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	65	70	75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	80	85	90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	95	100	105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	110	115	120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	125	130	135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	140	145	150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	155	160	165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	170	175	180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	185	190	195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	200	205	210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	215	220	225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	230	235	240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	245	250	255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala				

260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro		
275	280	285
Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu		
290	295	300
Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly		
305	310	315
Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu		
320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg		
335	340	345
Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp		
350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr		
365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu		
380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg		
395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val		
410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser		
425	430	435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val		
440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala		
455	460	465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro		
470	475	480
Thr Phe Thr Gln Trp Leu Cys		
485		

<210> 64

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 65

gtcacacaca gctctggcag ctgag 25

<210> 66

<211> 47

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-47

<223> Synthetic construct.

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

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ggcccagcaa gcctgataag catgaagctc ttatcttttg tggctgtggt 150
cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200
tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300
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 ttttatctct ctca 1564

<210> 68
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 68
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
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 Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
 20 25 30
 Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
 35 40 45
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
 50 55 60

Pro	Met	Pro	Val	Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu	65	70	75
Cys	Glu	Cys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val	80	85	90
Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr	95	100	105
Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp	110	115	120
Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	Glu	Glu	Glu	Asn	Glu	Asp	Ala	125	130	135
Arg	Ser	Met	Ala	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala	140	145	150
Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys	155	160	165
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys	170	175	180
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<210> 69
 <211> 3170
 <212> DNA
 <213> Homo sapiens

<400> 69
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 tccctttgca tccccacccc tccgggcttt gcgtcttctt ggggaccccc 200
 tcgccgggag atggcgcggt tgatgcggag caaggattcg tctgtctgcc 250
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<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

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Leu	Leu	Ala	Ala	Val	Leu	Met	Val	Glu	Ser	Ser	Gln	Ile	Gly	Ser
				20					25				30	

Ser	Arg	Ala	Lys	Leu	Asn	Ser	Ile	Lys	Ser	Ser	Leu	Gly	Gly	Glu
				35					40				45	

Thr	Pro	Gly	Gln	Ala	Ala	Asn	Arg	Ser	Ala	Gly	Met	Tyr	Gln	Gly	
				50					55					60	
Leu	Ala	Phe	Gly	Gly	Ser	Lys	Lys	Gly	Lys	Asn	Leu	Gly	Gln	Ala	
				65					70					75	
Tyr	Pro	Cys	Ser	Ser	Asp	Lys	Glu	Cys	Glu	Val	Gly	Arg	Tyr	Cys	
				80					85					90	
His	Ser	Pro	His	Gln	Gly	Ser	Ser	Ala	Cys	Met	Val	Cys	Arg	Arg	
				95					100					105	
Lys	Lys	Lys	Arg	Cys	His	Arg	Asp	Gly	Met	Cys	Cys	Pro	Ser	Thr	
				110					115					120	
Arg	Cys	Asn	Asn	Gly	Ile	Cys	Ile	Pro	Val	Thr	Glu	Ser	Ile	Leu	
				125					130					135	
Thr	Pro	His	Ile	Pro	Ala	Leu	Asp	Gly	Thr	Arg	His	Arg	Asp	Arg	
				140					145					150	
Asn	His	Gly	His	Tyr	Ser	Asn	His	Asp	Leu	Gly	Trp	Gln	Asn	Leu	
				155					160					165	
Gly	Arg	Pro	His	Thr	Lys	Met	Ser	His	Ile	Lys	Gly	His	Glu	Gly	
				170					175					180	
Asp	Pro	Cys	Leu	Arg	Ser	Ser	Asp	Cys	Ile	Glu	Gly	Phe	Cys	Cys	
				185					190					195	
Ala	Arg	His	Phe	Trp	Thr	Lys	Ile	Cys	Lys	Pro	Val	Leu	His	Gln	
				200					205					210	
Gly	Glu	Val	Cys	Thr	Lys	Gln	Arg	Lys	Lys	Gly	Ser	His	Gly	Leu	
				215					220					225	
Glu	Ile	Phe	Gln	Arg	Cys	Asp	Cys	Ala	Lys	Gly	Leu	Ser	Cys	Lys	
				230					235					240	
Val	Trp	Lys	Asp	Ala	Thr	Tyr	Ser	Ser	Lys	Ala	Arg	Leu	His	Val	
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Cys Gln Lys Ile

<210> 71

<211> 1809

<212> DNA

<213> Homo sapiens

<400> 71

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acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150

cttccttcta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200

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atatttttagt aattcatatg ttttagatta taggttttaa cataacttggtg 300
aaaataacttg atgtgtttta aagccttggg cagaaattct gtattgttga 350
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 ctgaaaaga 1809

<210> 72
 <211> 363
 <212> PRT
 <213> Homo sapiens

<400> 72

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Cys	Ser	Phe	Ile	Pro	Leu	Leu	Lys	Ser	Ser	Val	Leu	Gly	Ser	Gly	
				20					25					30	
Phe	Gly	Glu	Leu	Ala	Pro	Pro	Lys	Met	Ala	Asn	Ile	Thr	Ser	Ser	
				35					40					45	
Gln	Ile	Leu	Asp	Gln	Leu	Lys	Ala	Pro	Ser	Leu	Gly	Gln	Phe	Thr	
				50					55					60	
Thr	Thr	Pro	Ser	Thr	Gln	Gln	Asn	Ser	Thr	Ser	His	Pro	Thr	Thr	
				65					70					75	
Thr	Thr	Ser	Trp	Asp	Leu	Lys	Pro	Pro	Thr	Ser	Gln	Ser	Ser	Val	
				80					85					90	
Leu	Ser	His	Leu	Asp	Phe	Lys	Ser	Gln	Pro	Glu	Pro	Ser	Pro	Val	
				95					100					105	
Leu	Ser	Gln	Leu	Ser	Gln	Arg	Gln	Gln	His	Gln	Ser	Gln	Ala	Val	
				110					115					120	
Thr	Val	Pro	Pro	Pro	Gly	Leu	Glu	Ser	Phe	Pro	Ser	Gln	Ala	Lys	
				125					130					135	
Leu	Arg	Glu	Ser	Thr	Pro	Gly	Asp	Ser	Pro	Ser	Thr	Val	Asn	Lys	
				140					145					150	
Leu	Leu	Gln	Leu	Pro	Ser	Thr	Thr	Ile	Glu	Asn	Ile	Ser	Val	Ser	
				155					160					165	
Val	His	Gln	Pro	Gln	Pro	Lys	His	Ile	Lys	Leu	Ala	Lys	Arg	Arg	
				170					175					180	
Ile	Pro	Pro	Ala	Ser	Lys	Ile	Pro	Ala	Ser	Ala	Val	Glu	Met	Pro	
				185					190					195	
Gly	Ser	Ala	Asp	Val	Thr	Gly	Leu	Asn	Val	Gln	Phe	Gly	Ala	Leu	
				200					205					210	
Glu	Phe	Gly	Ser	Glu	Pro	Ser	Leu	Ser	Glu	Phe	Gly	Ser	Ala	Pro	
				215					220					225	

Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser
				275					280					285
Ser	Ser	Tyr	Asp	Gln	Ser	Ser	Val	His	Asn	Arg	Ile	Pro	Tyr	Gln
				290					295					300
Ser	Pro	Val	Ser	Ser	Ser	Glu	Ser	Ala	Pro	Gly	Thr	Ile	Met	Asn
				305					310					315
Gly	His	Gly	Gly	Gly	Arg	Ser	Gln	Gln	Thr	Leu	Asp	Ser	Lys	Tyr
				320					325					330
Ser	Ser	Lys	Leu	Leu	Leu	Ser	Trp	Leu	Val	Pro	Thr	Lys	Gln	Arg
				335					340					345
Lys	Arg	Ile	Ala	His	Val	Met	Trp	Lys	Thr	Pro	Val	Gly	Gln	Trp
				350					355					360

Leu Ile Arg

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 73
 aattcatggc aaatatttcc cttccc 26

<210> 74
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 74
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<210> 75
 <211> 50

<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
ttaaagtcac ccgtccttgg ctcaggattt ggagagcttg caccacccaaa 50

<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
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caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77

<211> 341

<212> PRT

<213> Homo sapiens

<400> 77

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Gln	Ser	Ser	Ala	Val	Leu	Leu	His	Ser	Ala	Val	Glu	Glu	Thr	Asp
				20					25					30

Ala	Gly	Leu	Tyr	Thr	Cys	Asn	Leu	His	His	His	Tyr	Cys	His	Leu
				35				40						45

Tyr	Glu	Ser	Leu	Ala	Val	Arg	Leu	Glu	Val	Thr	Asp	Gly	Pro	Pro
				50				55						60

Ala	Thr	Pro	Ala	Tyr	Trp	Asp	Gly	Glu	Lys	Glu	Val	Leu	Ala	Val
				65				70						75

Ala Arg Gly Ala	Pro	Ala	Leu	Leu	Thr	Cys	Val	Asn	Arg	Gly	His
	80					85					90
Val Trp Thr Asp	Arg	His	Val	Glu	Glu	Ala	Gln	Gln	Val	Val	His
	95					100					105
Trp Asp Arg Gln	Pro	Pro	Gly	Val	Pro	His	Asp	Arg	Ala	Asp	Arg
	110					115					120
Leu Leu Asp Leu	Tyr	Ala	Ser	Gly	Glu	Arg	Arg	Ala	Tyr	Gly	Pro
	125					130					135
Leu Phe Leu Arg	Asp	Arg	Val	Ala	Val	Gly	Ala	Asp	Ala	Phe	Glu
	140					145					150
Arg Gly Asp Phe	Ser	Leu	Arg	Ile	Glu	Pro	Leu	Glu	Val	Ala	Asp
	155					160					165
Glu Gly Thr Tyr	Ser	Cys	His	Leu	His	His	His	Tyr	Cys	Gly	Leu
	170					175					180
His Glu Arg Arg	Val	Phe	His	Leu	Thr	Val	Ala	Glu	Pro	His	Ala
	185					190					195
Glu Pro Pro Pro	Arg	Gly	Ser	Pro	Gly	Asn	Gly	Ser	Ser	His	Ser
	200					205					210
Gly Ala Pro Gly	Pro	Asp	Pro	Thr	Leu	Ala	Arg	Gly	His	Asn	Val
	215					220					225
Ile Asn Val Ile	Val	Pro	Glu	Ser	Arg	Ala	His	Phe	Phe	Gln	Gln
	230					235					240
Leu Gly Tyr Val	Leu	Ala	Thr	Leu	Leu	Leu	Phe	Ile	Leu	Leu	Leu
	245					250					255
Val Thr Val Leu	Leu	Ala	Ala	Arg	Arg	Arg	Arg	Gly	Gly	Tyr	Glu
	260					265					270
Tyr Ser Asp Gln	Lys	Ser	Gly	Lys	Ser	Lys	Gly	Lys	Asp	Val	Asn
	275					280					285
Leu Ala Glu Phe	Ala	Val	Ala	Ala	Gly	Asp	Gln	Met	Leu	Tyr	Arg
	290					295					300
Ser Glu Asp Ile	Gln	Leu	Asp	Tyr	Lys	Asn	Asn	Ile	Leu	Lys	Glu
	305					310					315
Arg Ala Glu Leu	Ala	His	Ser	Pro	Leu	Pro	Ala	Lys	Tyr	Ile	Asp
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Leu Asp Lys Gly	Phe	Arg	Lys	Glu	Asn	Cys	Lys				
	335					340					

<210> 78
 <211> 2243
 <212> DNA
 <213> Homo sapiens

<400> 78

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<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

Met	Ala	Val	Val	Ser	Glu	Asp	Asp	Phe	Gln	His	Ser	Ser	Asn	Ser
1				5					10					15

Thr	Tyr	Gly	Thr	Thr	Ser	Ser	Ser	Leu	Arg	Ala	Asp	Gln	Glu	Ala
				20					25					30

Leu	Leu	Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Pro	Gly	Leu	Gln	Arg
			35						40					45

Pro	Glu	Asp	Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu
			50						55					60

Gly	Ile	Gly	Ser	Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys
			65						70					75

Glu	Tyr	Trp	Met	Phe	Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr
			80						85					90

Gly	Glu	Asp	Pro	Glu	Gly	Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser
			95						100					105

Tyr Leu Ala Val	Ala Ser Thr Val	Pro Ser Met Leu Cys Leu Val	110	115	120
Ala Asn Phe Leu	Leu Val Asn Arg Val	Ala Val His Ile Arg Val	125	130	135
Leu Ala Ser Leu	Thr Val Ile Leu Ala	Ile Phe Met Val Ile Thr	140	145	150
Ala Leu Val Lys	Val Asp Thr Ser Ser	Trp Thr Arg Gly Phe Phe	155	160	165
Ala Val Thr Ile	Val Cys Met Val Ile	Leu Ser Gly Ala Ser Thr	170	175	180
Val Phe Ser Ser	Ser Ile Tyr Gly Met	Thr Gly Ser Phe Pro Met	185	190	195
Arg Asn Ser Gln	Ala Leu Ile Ser Gly	Gly Ala Met Gly Gly Thr	200	205	210
Val Ser Ala Val	Ala Ser Leu Val Asp	Leu Ala Ala Ser Ser Asp	215	220	225
Val Arg Asn Ser	Ala Leu Ala Phe Phe	Leu Thr Ala Thr Ile Phe	230	235	240
Leu Val Leu Cys	Met Gly Leu Tyr Leu	Leu Leu Ser Arg Leu Glu	245	250	255
Tyr Ala Arg Tyr	Tyr Met Arg Pro Val	Leu Ala Ala His Val Phe	260	265	270
Ser Gly Glu Glu	Glu Leu Pro Gln Asp	Ser Leu Ser Ala Pro Ser	275	280	285
Val Ala Ser Arg	Phe Ile Asp Ser His	Thr Pro Pro Leu Arg Pro	290	295	300
Ile Leu Lys Lys	Thr Ala Ser Leu Gly	Phe Cys Val Thr Tyr Val	305	310	315
Phe Phe Ile Thr	Ser Leu Ile Tyr Pro	Ala Val Cys Thr Asn Ile	320	325	330
Glu Ser Leu Asn	Lys Gly Ser Gly Ser	Leu Trp Thr Thr Lys Phe	335	340	345
Phe Ile Pro Leu	Thr Thr Phe Leu Leu	Tyr Asn Phe Ala Asp Leu	350	355	360
Cys Gly Arg Gln	Leu Thr Ala Trp Ile	Gln Val Pro Gly Pro Asn	365	370	375
Ser Lys Ala Leu	Pro Gly Phe Val Leu	Leu Arg Thr Cys Leu Ile	380	385	390
Pro Leu Phe Val	Leu Cys Asn Tyr Gln	Pro Arg Val His Leu Lys			

395	400	405
Thr Val Val Phe Gln Ser Asp Val Tyr	Pro Ala Leu Leu Ser Ser	
410	415	420
Leu Leu Gly Leu Ser Asn Gly Tyr Leu	Ser Thr Leu Ala Leu Leu	
425	430	435
Tyr Gly Pro Lys Ile Val Pro Arg Glu	Leu Ala Glu Ala Thr Gly	
440	445	450
Val Val Met Ser Phe Tyr Val Cys Leu	Gly Leu Thr Leu Gly Ser	
455	460	465
Ala Cys Ser Thr Leu Leu Val His Leu	Ile	
470	475	

<210> 80
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 80
 ttttgcggtc accattgtct gc 22

<210> 81
 <211> 23
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Artificial sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 81
 cgtaggtgac acagaagccc agg 23

<210> 82
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-49
 <223> Synthetic construct.

<400> 82
 tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83
 <211> 1844

<212> DNA

<213> Homo sapiens

<400> 83

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aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200
ctatgagcag ctgctcaagg tggtagcctg ggggctcaat cggaccctga 250
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gccaaggtgc tcagcgatgc tggacacaag gtcaccatcc tggaggcaga 350
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ggattgggga gctgggagcc atgcgcatgc ccagctctca caggatcctc 450
cacaagctct gccagggcct ggggctcaac ctgaccaagt tcaccagta 500
cgacaagaac acgtggacgg aggtgcacga agtgaagctg cgcaactatg 550
tggtaggaga ggtgcccag aagctgggct acgccttgcg tcccaggaa 600
aagggccact cgcccgaaga catctaccag atggctctca accaggccct 650
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ggcacacgct cttggaatat cttctcgggg aggggaacct gagccggccg 750
gccgtgcagc ttctgggaga cgtgatgtcc gaggatggct tcttctatct 800
cagcttcgcc gagggccctc gggccacag ctgcctcagc gacagactcc 850
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aacacgatc gcccgtcgcg catgattttc taccgcccgc cgcgagagg 1250
cgcgctgctg ctggcctcgt acacgtggtc ggacggggcg gcagcgttcg 1300
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 ggcaaaggaa gaaggcagcc accctccagt ccaaggccag ttatctctcc 1750
 aaaacacgac ccacacgagg acctcgcat aaagtatttt cggaaaaaaaa 1800
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84

<211> 567

<212> PRT

<213> Homo sapiens

<400> 84

Met	Ala	Pro	Leu	Ala	Leu	His	Leu	Leu	Val	Leu	Val	Pro	Ile	Leu	1	5	10	15
Leu	Ser	Leu	Val	Ala	Ser	Gln	Asp	Trp	Lys	Ala	Glu	Arg	Ser	Gln	20	25	30	
Asp	Pro	Phe	Glu	Lys	Cys	Met	Gln	Asp	Pro	Asp	Tyr	Glu	Gln	Leu	35	40	45	
Leu	Lys	Val	Val	Thr	Trp	Gly	Leu	Asn	Arg	Thr	Leu	Lys	Pro	Gln	50	55	60	
Arg	Val	Ile	Val	Val	Gly	Ala	Gly	Val	Ala	Gly	Leu	Val	Ala	Ala	65	70	75	
Lys	Val	Leu	Ser	Asp	Ala	Gly	His	Lys	Val	Thr	Ile	Leu	Glu	Ala	80	85	90	
Asp	Asn	Arg	Ile	Gly	Gly	Arg	Ile	Phe	Thr	Tyr	Arg	Asp	Gln	Asn	95	100	105	
Thr	Gly	Trp	Ile	Gly	Glu	Leu	Gly	Ala	Met	Arg	Met	Pro	Ser	Ser	110	115	120	
His	Arg	Ile	Leu	His	Lys	Leu	Cys	Gln	Gly	Leu	Gly	Leu	Asn	Leu	125	130	135	
Thr	Lys	Phe	Thr	Gln	Tyr	Asp	Lys	Asn	Thr	Trp	Thr	Glu	Val	His	140	145	150	
Glu	Val	Lys	Leu	Arg	Asn	Tyr	Val	Val	Glu	Lys	Val	Pro	Glu	Lys	155	160	165	

Leu Gly Tyr Ala	Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu	170	175	180
Asp Ile Tyr Gln Met	Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys	185	190	195
Ala Leu Gly Cys Arg	Lys Ala Met Lys Lys Phe Glu Arg His Thr	200	205	210
Leu Leu Glu Tyr	Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala	215	220	225
Val Gln Leu Leu Gly	Asp Val Met Ser Glu Asp Gly Phe Phe Tyr	230	235	240
Leu Ser Phe Ala Glu	Ala Leu Arg Ala His Ser Cys Leu Ser Asp	245	250	255
Arg Leu Gln Tyr Ser	Arg Ile Val Gly Gly Trp Asp Leu Leu Pro	260	265	270
Arg Ala Leu Leu Ser	Ser Leu Ser Gly Leu Val Leu Leu Asn Ala	275	280	285
Pro Val Val Ala Met	Thr Gln Gly Pro His Asp Val His Val Gln	290	295	300
Ile Glu Thr Ser Pro	Pro Ala Arg Asn Leu Lys Val Leu Lys Ala	305	310	315
Asp Val Val Leu Leu	Thr Ala Ser Gly Pro Ala Val Lys Arg Ile	320	325	330
Thr Phe Ser Pro Pro	Leu Pro Arg His Met Gln Glu Ala Leu Arg	335	340	345
Arg Leu His Tyr Val	Pro Ala Thr Lys Val Phe Leu Ser Phe Arg	350	355	360
Arg Pro Phe Trp Arg	Glu Glu His Ile Glu Gly Gly His Ser Asn	365	370	375
Thr Asp Arg Pro Ser	Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu	380	385	390
Gly Ala Leu Leu Leu	Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala	395	400	405
Ala Phe Ala Gly Leu	Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu	410	415	420
Asp Asp Val Ala Ala	Leu His Gly Pro Val Val Arg Gln Leu Trp	425	430	435
Asp Gly Thr Gly Val	Val Lys Arg Trp Ala Glu Asp Gln His Ser	440	445	450
Gln Gly Gly Phe Val	Val Gln Pro Pro Ala Leu Trp Gln Thr Glu			

455	460	465
Lys Asp Asp Trp Thr Val Pro Tyr Gly	Arg Ile Tyr Phe Ala Gly	
470	475	480
Glu His Thr Ala Tyr Pro His Gly Trp	Val Glu Thr Ala Val Lys	
485	490	495
Ser Ala Leu Arg Ala Ala Ile Lys Ile	Asn Ser Arg Lys Gly Pro	
500	505	510
Ala Ser Asp Thr Ala Ser Pro Glu Gly	His Ala Ser Asp Met Glu	
515	520	525
Gly Gln Gly His Val His Gly Val Ala	Ser Ser Pro Ser His Asp	
530	535	540
Leu Ala Lys Glu Glu Gly Ser His Pro	Pro Val Gln Gly Gln Leu	
545	550	555
Ser Leu Gln Asn Thr Thr His Thr Arg	Thr Ser His	
560	565	

<210> 85
 <211> 3316
 <212> DNA
 <213> Homo sapiens

<400> 85
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 tggaggaacc acgagcgagg gaagaaggac agggactcgt gtggcaggaa 150
 gaactcagag ccgggaagcc ccatttcaact agaagcactg agagatgcgg 200
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 cctgacattt ggagctgccca ttttcttctg gctgatcacc agacctcaac 350
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<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

Met	Asp	Ala	Leu	Lys	Pro	Pro	Cys	Leu	Trp	Arg	Asn	His	Glu	Arg
1				5					10					15

Gly	Lys	Lys	Asp	Arg	Asp	Ser	Cys	Gly	Arg	Lys	Asn	Ser	Glu	Pro
			20						25					30

Gly Ser Pro His	Ser Leu Glu Ala Leu Arg Asp Ala Ala Pro Ser	35	40	45
Gln Gly Leu Asn Phe Leu Leu Leu Phe Thr Lys Met Leu Phe Ile		50	55	60
Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala Leu Ile Cys		65	70	75
Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile Thr Arg		80	85	90
Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser Val		95	100	105
Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn		110	115	120
Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu		125	130	135
Val Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu		140	145	150
Gly Tyr Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys		155	160	165
Gln Val Ser Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His		170	175	180
Lys Gly Tyr Lys Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala		185	190	195
Gln Asn Arg Pro Glu Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr		200	205	210
Tyr Ser Met Val Ala Val Pro Leu Tyr Asp Thr Leu Gly Pro Glu		215	220	225
Ala Ile Val His Ile Val Asn Lys Ala Asp Ile Ala Met Val Ile		230	235	240
Cys Asp Thr Pro Gln Lys Ala Leu Val Leu Ile Gly Asn Val Glu		245	250	255
Lys Gly Phe Thr Pro Ser Leu Lys Val Ile Ile Leu Met Asp Pro		260	265	270
Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu Lys Ser Gly Ile Glu		275	280	285
Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Gly Lys Glu His Phe		290	295	300
Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser Val Ile Cys		305	310	315
Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met Ile Thr				

320	325	330
His Gln Asn Ile Val Ser Asn Ala Ala	Ala Phe Leu Lys Cys Val	
335	340	345
Glu His Ala Tyr Glu Pro Thr Pro Asp	Asp Val Ala Ile Ser Tyr	
350	355	360
Leu Pro Leu Ala His Met Phe Glu Arg	Ile Val Gln Ala Val Val	
365	370	375
Tyr Ser Cys Gly Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile Arg	
380	385	390
Leu Leu Ala Asp Asp Met Lys Thr Leu	Lys Pro Thr Leu Phe Pro	
395	400	405
Ala Val Pro Arg Leu Leu Asn Arg Ile	Tyr Asp Lys Val Gln Asn	
410	415	420
Glu Ala Lys Thr Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala Val	
425	430	435
Ser Ser Lys Phe Lys Glu Leu Gln Lys	Gly Ile Ile Arg His Asp	
440	445	450
Ser Phe Trp Asp Lys Leu Ile Phe Ala	Lys Ile Gln Asp Ser Leu	
455	460	465
Gly Gly Arg Val Arg Val Ile Val Thr	Gly Ala Ala Pro Met Ser	
470	475	480
Thr Ser Val Met Thr Phe Phe Arg Ala	Ala Met Gly Cys Gln Val	
485	490	495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys	Thr Gly Gly Cys Thr Phe	
500	505	510
Thr Leu Pro Gly Asp Trp Thr Ser Gly	His Val Gly Val Pro Leu	
515	520	525
Ala Cys Asn Tyr Val Lys Leu Glu Asp	Val Ala Asp Met Asn Tyr	
530	535	540
Phe Thr Val Asn Asn Glu Gly Glu Val	Cys Ile Lys Gly Thr Asn	
545	550	555
Val Phe Lys Gly Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu Ala	
560	565	570
Leu Asp Ser Asp Gly Trp Leu His Thr	Gly Asp Ile Gly Arg Trp	
575	580	585
Leu Pro Asn Gly Thr Leu Lys Ile Ile	Asp Arg Lys Lys Asn Ile	
590	595	600
Phe Lys Leu Ala Gln Gly Glu Tyr Ile	Ala Pro Glu Lys Ile Glu	
605	610	615

Asn	Ile	Tyr	Asn	Arg	Ser	Gln	Pro	Val	Leu	Gln	Ile	Phe	Val	His
				620					625					630
Gly	Glu	Ser	Leu	Arg	Ser	Ser	Leu	Val	Gly	Val	Val	Val	Pro	Asp
				635					640					645
Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
				650					655					660
Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
				665					670					675
Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
				680					685					690
Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
				695					700					705
Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
				710					715					720
Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr	Gln	Ile	Asp	Ser	Leu	Tyr	Glu
				725					730					735

His Ile Gln Asp

<210> 87
 <211> 2725
 <212> DNA
 <213> Homo sapiens

<400> 87
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 cccctcatca agcccttttg ggctcggaag aagcggagct ggtaccttac 200
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 aaaaaaaaaa aaaaaaaaaa aaaaa 2725

<210> 88

<211> 660

<212> PRT

<213> Homo sapiens

<400> 88

Met	Asp	Asp	Trp	Lys	Pro	Ser	Pro	Leu	Ile	Lys	Pro	Phe	Gly	Ala	1	5	10	15
Arg	Lys	Lys	Arg	Ser	Trp	Tyr	Leu	Thr	Trp	Lys	Tyr	Lys	Leu	Thr	20	25	30	
Asn	Gln	Arg	Ala	Leu	Arg	Arg	Phe	Cys	Gln	Thr	Gly	Ala	Val	Leu	35	40	45	
Phe	Leu	Leu	Val	Thr	Val	Ile	Val	Asn	Ile	Lys	Leu	Ile	Leu	Asp	50	55	60	
Thr	Arg	Arg	Ala	Ile	Ser	Glu	Ala	Asn	Glu	Asp	Pro	Glu	Pro	Glu	65	70	75	
Gln	Asp	Tyr	Asp	Glu	Ala	Leu	Gly	Arg	Leu	Glu	Pro	Pro	Arg	Arg	80	85	90	
Arg	Gly	Ser	Gly	Pro	Arg	Arg	Val	Leu	Asp	Val	Glu	Val	Tyr	Ser	95	100	105	
Ser	Arg	Ser	Lys	Val	Tyr	Val	Ala	Val	Asp	Gly	Thr	Thr	Val	Leu	110	115	120	
Glu	Asp	Glu	Ala	Arg	Glu	Gln	Gly	Arg	Gly	Ile	His	Val	Ile	Val	125	130	135	

Leu Asn Gln Ala Thr Gly His Val Met	Ala Lys Arg Val Phe Asp	140	145	150
Thr Tyr Ser Pro His Glu Asp Glu Ala Met	Val Leu Phe Leu Asn	155	160	165
Met Val Ala Pro Gly Arg Val Leu Ile Cys	Thr Val Lys Asp Glu	170	175	180
Gly Ser Phe His Leu Lys Asp Thr Ala Lys	Ala Leu Leu Arg Ser	185	190	195
Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly	Trp Arg Asp Thr Trp	200	205	210
Ala Phe Val Gly Arg Lys Gly Gly Pro Val	Phe Gly Glu Lys His	215	220	225
Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly	Asp Pro Val Leu Leu	230	235	240
Lys Thr Asp Val Pro Leu Ser Ser Ala Glu	Glu Ala Glu Cys His	245	250	255
Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg	Arg Arg Arg Phe Cys Ser	260	265	270
Lys Val Glu Gly Tyr Gly Ser Val Cys Ser	Cys Lys Asp Pro Thr	275	280	285
Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro	Asp Asn Lys Val Leu	290	295	300
Asn Val Pro Val Ala Val Ile Ala Gly Asn	Arg Pro Asn Tyr Leu	305	310	315
Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala	Gln Gly Val Ser Pro	320	325	330
Gln Met Ile Thr Val Phe Ile Asp Gly Tyr	Tyr Glu Glu Pro Met	335	340	345
Asp Val Val Ala Leu Phe Gly Leu Arg Gly	Ile Gln His Thr Pro	350	355	360
Ile Ser Ile Lys Asn Ala Arg Val Ser Gln	His Tyr Lys Ala Ser	365	370	375
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu	Ala Lys Phe Ala Val	380	385	390
Val Leu Glu Glu Asp Leu Asp Ile Ala Val	Asp Phe Phe Ser Phe	395	400	405
Leu Ser Gln Ser Ile His Leu Leu Glu Glu	Asp Asp Ser Leu Tyr	410	415	420
Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr	Glu His Thr Ala Glu			

425	430	435
Asp Pro Ala Leu Leu Tyr Arg Val Glu Thr Met Pro Gly Leu Gly		
440	445	450
Trp Val Leu Arg Arg Ser Leu Tyr Lys Glu Glu Leu Glu Pro Lys		
455	460	465
Trp Pro Thr Pro Glu Lys Leu Trp Asp Trp Asp Met Trp Met Arg		
470	475	480
Met Pro Glu Gln Arg Arg Gly Arg Glu Cys Ile Ile Pro Asp Val		
485	490	495
Ser Arg Ser Tyr His Phe Gly Ile Val Gly Leu Asn Met Asn Gly		
500	505	510
Tyr Phe His Glu Ala Tyr Phe Lys Lys His Lys Phe Asn Thr Val		
515	520	525
Pro Gly Val Gln Leu Arg Asn Val Asp Ser Leu Lys Lys Glu Ala		
530	535	540
Tyr Glu Val Glu Val His Arg Leu Leu Ser Glu Ala Glu Val Leu		
545	550	555
Asp His Ser Lys Asn Pro Cys Glu Asp Ser Phe Leu Pro Asp Thr		
560	565	570
Glu Gly His Thr Tyr Val Ala Phe Ile Arg Met Glu Lys Asp Asp		
575	580	585
Asp Phe Thr Thr Trp Thr Gln Leu Ala Lys Cys Leu His Ile Trp		
590	595	600
Asp Leu Asp Val Arg Gly Asn His Arg Gly Leu Trp Arg Leu Phe		
605	610	615
Arg Lys Lys Asn His Phe Leu Val Val Gly Val Pro Ala Ser Pro		
620	625	630
Tyr Ser Val Lys Lys Pro Pro Ser Val Thr Pro Ile Phe Leu Glu		
635	640	645
Pro Pro Pro Lys Glu Glu Gly Ala Pro Gly Ala Pro Glu Gln Thr		
650	655	660

<210> 89

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 89

gatggcaaaa cgtgtgtttg acacg 25

<210> 90
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 90
cctcaaccag gccacgggcc ac 22

<210> 91
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 91
cccaggcaga gatgcagtac aggc 24

<210> 92
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 92
cctccagtag gtggatggat tggctc 26

<210> 93
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-47
<223> Synthetic construct.

<400> 93
ctcacctcat gaggatgagg ccatggtgct attcctcaac atggtag 47

<210> 94
<211> 3037
<212> DNA
<213> Homo sapiens

<400> 94

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ctcttggaac caccacacct gtttaaagaa cctaagcacc atttaaagcc 100
actggaaatt tgttgtctag tgggtgtggg tgaataaagg agggcagaat 150
ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtgggat 200
gttacgtggc cggaatcatt cccttggctg ttaatttctc agaggaacga 250
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agggaaaaca ccaccaagca agtgaaacac ataatgtgat tgcacagac 400
aaagcagcag aaaaatcagt tgtccatgaa catgagcaca gccacgacca 450
cacacagctg catgcctata ttggtgtttc cctcgttctg ggcttcgttt 500
tcatgttgct ggtggaccag attggttaact cccatgtgca ttctactgac 550
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<210> 95
 <211> 307
 <212> PRT
 <213> Homo sapiens

<400> 95

Met	Asp	Asp	Phe	Ile	Ser	Ile	Ser	Leu	Leu	Ser	Leu	Ala	Met	Leu	1	5	10	15
Val	Gly	Cys	Tyr	Val	Ala	Gly	Ile	Ile	Pro	Leu	Ala	Val	Asn	Phe	20	25	30	
Ser	Glu	Glu	Arg	Leu	Lys	Leu	Val	Thr	Val	Leu	Gly	Ala	Gly	Leu	35	40	45	
Leu	Cys	Gly	Thr	Ala	Leu	Ala	Val	Ile	Val	Pro	Glu	Gly	Val	His	50	55	60	
Ala	Leu	Tyr	Glu	Asp	Ile	Leu	Glu	Gly	Lys	His	His	Gln	Ala	Ser	65	70	75	
Glu	Thr	His	Asn	Val	Ile	Ala	Ser	Asp	Lys	Ala	Ala	Glu	Lys	Ser	80	85	90	
Val	Val	His	Glu	His	Glu	His	Ser	His	Asp	His	Thr	Gln	Leu	His	95	100	105	
Ala	Tyr	Ile	Gly	Val	Ser	Leu	Val	Leu	Gly	Phe	Val	Phe	Met	Leu	110	115	120	
Leu	Val	Asp	Gln	Ile	Gly	Asn	Ser	His	Val	His	Ser	Thr	Asp	Asp	125	130	135	
Pro	Glu	Ala	Ala	Arg	Ser	Ser	Asn	Ser	Lys	Ile	Thr	Thr	Thr	Leu	140	145	150	
Gly	Leu	Val	Val	His	Ala	Ala	Ala	Asp	Gly	Val	Ala	Leu	Gly	Ala	155	160	165	
Ala	Ala	Ser	Thr	Ser	Gln	Thr	Ser	Val	Gln	Leu	Ile	Val	Phe	Val	170	175	180	
Ala	Ile	Met	Leu	His	Lys	Ala	Pro	Ala	Ala	Phe	Gly	Leu	Val	Ser	185	190	195	
Phe	Leu	Met	His	Ala	Gly	Leu	Glu	Arg	Asn	Arg	Ile	Arg	Lys	His	200	205	210	
Leu	Leu	Val	Phe	Ala	Leu	Ala	Ala	Pro	Val	Met	Ser	Met	Val	Thr	215	220	225	
Tyr	Leu	Gly	Leu	Ser	Lys	Ser	Ser	Lys	Glu	Ala	Leu	Ser	Glu	Val				

230	235	240
Asn Ala Thr Gly Val Ala Met Leu Phe	Ser Ala Gly Thr Phe Leu	
245	250	255
Tyr Val Ala Thr Val His Val Leu Pro	Glu Val Gly Gly Ile Gly	
260	265	270
His Ser His Lys Pro Asp Ala Thr Gly	Gly Arg Gly Leu Ser Arg	
275	280	285
Leu Glu Val Ala Ala Leu Val Leu Gly	Cys Leu Ile Pro Leu Ile	
290	295	300
Leu Ser Val Gly His Gln His		
305		

<210> 96
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 96
 gttgtgggtg aataaaggag ggcag 25

<210> 97
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 97
 ctgtgctcat gttcatggac aactg 25

<210> 98
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 98
 ggatgatttc atctccatta gctgtctgtc tctggctatg ttggtgggat 50

<210> 99
 <211> 1429

<212> DNA

<213> Homo sapiens

<400> 99

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gccccggatc cccgagtggc ggccggagcc tcgaaaagag attctcagcg 100
ctgattttga gatgatgggc ttgggaaacg ggcgtcgcag catgaagtcg 150
ccgcccctcg tgctggccgc cctggtggcc tgcacatcg tcttgggctt 200
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gaaatgtact aaataaaatg tacatctga 1429

<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

Met Met Gly Leu Gly Asn Gly Arg Arg Ser Met Lys Ser Pro Pro
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Leu Val Leu Ala Ala Leu Val Ala Cys Ile Ile Val Leu Gly Phe
20 25 30

Asn Tyr Trp Ile Ala Ser Ser Arg Ser Val Asp Leu Gln Thr Arg
35 40 45

Ile Met Glu Leu Glu Gly Arg Val Arg Arg Ala Ala Ala Glu Arg
50 55 60

Gly Ala Val Glu Leu Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu
65 70 75

Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser Ser His Asn Phe
80 85 90

Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu Lys Ala Val
95 100 105

Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg Val Leu
110 115 120

Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu Gln
125 130 135

Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg
140 145 150

Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu
155 160 165

Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys
170 175 180

Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp
185 190 195

Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu
200 205 210

Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly
215 220 225

Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser
230 235 240

Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr	245	250	255
Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu	260	265	270
Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val	275	280	285
Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro	290	295	300
Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met	305	310	315
Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu	320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu	335	340	345
Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser	350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile	365	370	375
Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu	380	385	390
Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu	395	400	

<210> 101
 <211> 3671
 <212> DNA
 <213> Homo sapiens

<400> 101
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<210> 102

<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

Met	Gln	Lys	Ala	Ser	Val	Leu	Leu	Phe	Leu	Ala	Trp	Val	Cys	Phe
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Leu	Phe	Tyr	Ala	Gly	Ile	Ala	Leu	Phe	Thr	Ser	Gly	Phe	Leu	Leu
				20					25					30
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro
				35					40					45
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala
				50					55					60
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile
				65					70					75
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val
				80					85					90
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser
				95					100					105
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu
				110					115					120
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu
				125					130					135
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly
				140					145					150
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys
				155					160					165
Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp
				170					175					180
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe
				185					190					195
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly

	200	205	210
Ile Leu Glu His	Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp	Asp
	215	220	225
Val Leu Ile Ala	His Phe Leu Gly Val	Asp His Cys Gly His	Lys
	230	235	240
His Gly Pro His	His Pro Glu Met Ala	Lys Lys Leu Ser Gln	Met
	245	250	255
Asp Gln Val Ile	Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp	Thr
	260	265	270
Leu Leu Val Val	Ala Gly Asp His Gly	Met Thr Thr Asn Gly	Asp
	275	280	285
His Gly Gly Asp	Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe	Leu
	290	295	300
Tyr Ser Pro Thr	Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu	Pro
	305	310	315
Glu Val Ile Pro	Gln Val Ser Leu Val	Pro Thr Leu Ala Leu	Leu
	320	325	330
Leu Gly Leu Pro	Ile Pro Phe Gly Asn	Ile Gly Glu Val Met	Ala
	335	340	345
Glu Leu Phe Ser	Gly Gly Glu Asp Ser	Gln Pro His Ser Ser	Ala
	350	355	360
Leu Ala Gln Ala	Ser Ala Leu His Leu	Asn Ala Gln Gln Val	Ser
	365	370	375
Arg Phe Leu His	Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln	Ala
	380	385	390
Lys Glu Leu His	Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser	Ala
	395	400	405
Asp Tyr Gln Trp	Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala	Thr
	410	415	420
Leu Pro Thr Val	Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly	Ala
	425	430	435
Arg Ala Met Cys	Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val	Arg
	440	445	450
Met Ala Gly Gly	Thr Ala Leu Leu Ala	Ala Ser Cys Phe Ile	Cys
	455	460	465
Leu Leu Ala Ser	Gln Trp Ala Ile Ser	Pro Gly Phe Pro Phe	Cys
	470	475	480
Pro Leu Leu Leu	Thr Pro Val Ala Trp	Gly Leu Val Gly Ala	Ile
	485	490	495

Ala Tyr Ala Gly	Leu	Leu Gly Thr Ile	Glu	Leu Lys Leu Asp	Leu
	500		505		510
Val Leu Leu Gly	Ala Val Ala Ala Val	Ser Ser Phe Leu Pro	Phe		
	515		520		525
Leu Trp Lys Ala	Trp Ala Gly Trp Gly	Ser Lys Arg Pro Leu	Ala		
	530		535		540
Thr Leu Phe Pro	Ile Pro Gly Pro Val	Leu Leu Leu Leu Leu	Phe		
	545		550		555
Arg Leu Ala Val	Phe Phe Ser Asp Ser	Phe Val Val Ala Glu	Ala		
	560		565		570
Arg Ala Thr Pro	Phe Leu Leu Gly Ser	Phe Ile Leu Leu Leu	Val		
	575		580		585
Val Gln Leu His	Trp Glu Gly Gln Leu	Leu Pro Pro Lys Leu	Leu		
	590		595		600
Thr Met Pro Arg	Leu Gly Thr Ser Ala	Thr Thr Asn Pro Pro	Arg		
	605		610		615
His Asn Gly Ala	Tyr Ala Leu Arg Leu	Gly Ile Gly Leu Leu	Leu		
	620		625		630
Cys Thr Arg Leu	Ala Gly Leu Phe His	Arg Cys Pro Glu Glu	Thr		
	635		640		645
Pro Val Cys His	Ser Ser Pro Trp Leu	Ser Pro Leu Ala Ser	Met		
	650		655		660
Val Gly Gly Arg	Ala Lys Asn Leu Trp	Tyr Gly Ala Cys Val	Ala		
	665		670		675
Ala Leu Val Ala	Leu Leu Ala Ala Val	Arg Leu Trp Leu Arg	Arg		
	680		685		690
Tyr Gly Asn Leu	Lys Ser Pro Glu Pro	Pro Met Leu Phe Val	Arg		
	695		700		705
Trp Gly Leu Pro	Leu Met Ala Leu Gly	Thr Ala Ala Tyr Trp	Ala		
	710		715		720
Leu Ala Ser Gly	Ala Asp Glu Ala Pro	Pro Arg Leu Arg Val	Leu		
	725		730		735
Val Ser Gly Ala	Ser Met Val Leu Pro	Arg Ala Val Ala Gly	Leu		
	740		745		750
Ala Ala Ser Gly	Leu Ala Leu Leu Leu	Trp Lys Pro Val Thr	Val		
	755		760		765
Leu Val Lys Ala	Gly Ala Gly Ala Pro	Arg Thr Arg Thr Val	Leu		
	770		775		780
Thr Pro Phe Ser	Gly Pro Pro Thr Ser	Gln Ala Asp Leu Asp	Tyr		

785										790					795				
Val	Val	Pro	Gln	Ile	Tyr	Arg	His	Met	Gln	Glu	Glu	Phe	Arg	Gly					
				800					805					810					
Arg	Leu	Glu	Arg	Thr	Lys	Ser	Gln	Gly	Pro	Leu	Thr	Val	Ala	Ala					
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Tyr	Gln	Leu	Gly	Ser	Val	Tyr	Ser	Ala	Ala	Met	Val	Thr	Ala	Leu					
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Thr	Leu	Leu	Ala	Phe	Pro	Leu	Leu	Leu	Leu	His	Ala	Glu	Arg	Ile					
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Ser	Leu	Val	Phe	Leu	Leu	Leu	Phe	Leu	Gln	Ser	Phe	Leu	Leu	Leu					
				860					865					870					
His	Leu	Leu	Ala	Ala	Gly	Ile	Pro	Val	Thr	Thr	Pro	Gly	Pro	Phe					
				875					880					885					
Thr	Val	Pro	Trp	Gln	Ala	Val	Ser	Ala	Trp	Ala	Leu	Met	Ala	Thr					
				890					895					900					
Gln	Thr	Phe	Tyr	Ser	Thr	Gly	His	Gln	Pro	Val	Phe	Pro	Ala	Ile					
				905					910					915					
His	Trp	His	Ala	Ala	Phe	Val	Gly	Phe	Pro	Glu	Gly	His	Gly	Ser					
				920					925					930					
Cys	Thr	Trp	Leu	Pro	Ala	Leu	Leu	Val	Gly	Ala	Asn	Thr	Phe	Ala					
				935					940					945					
Ser	His	Leu	Leu	Phe	Ala	Val	Gly	Cys	Pro	Leu	Leu	Leu	Leu	Trp					
				950					955					960					
Pro	Phe	Leu	Cys	Glu	Ser	Gln	Gly	Leu	Arg	Lys	Arg	Gln	Gln	Pro					
				965					970					975					
Pro	Gly	Asn	Glu	Ala	Asp	Ala	Arg	Val	Arg	Pro	Glu	Glu	Glu	Glu					
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Glu	Pro	Leu	Met	Glu	Met	Arg	Leu	Arg	Asp	Ala	Pro	Gln	His	Phe					
				995					1000					1005					
Tyr	Ala	Ala	Leu	Leu	Gln	Leu	Gly	Leu	Lys	Tyr	Leu	Phe	Ile	Leu					
				1010					1015					1020					
Gly	Ile	Gln	Ile	Leu	Ala	Cys	Ala	Leu	Ala	Ala	Ser	Ile	Leu	Arg					
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Arg	His	Leu	Met	Val	Trp	Lys	Val	Phe	Ala	Pro	Lys	Phe	Ile	Phe					
				1040					1045					1050					
Glu	Ala	Val	Gly	Phe	Ile	Val	Ser	Ser	Val	Gly	Leu	Leu	Leu	Gly					
				1055					1060					1065					
Ile	Ala	Leu	Val	Met	Arg	Val	Asp	Gly	Ala	Val	Ser	Ser	Trp	Phe					
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Arg Gln Leu Phe Leu Ala Gln Gln Arg
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<210> 103

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 103

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<210> 104
 <211> 442
 <212> PRT
 <213> Homo sapiens

<400> 104
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 20 25 30
 Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr
 35 40 45
 Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser
 50 55 60
 Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu
 65 70 75
 Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His
 80 85 90
 Thr Leu Val Leu Thr Trp Leu Glu Pro Asn Thr Leu Tyr Cys Val
 95 100 105
 His Val Glu Ser Phe Val Pro Gly Pro Pro Arg Arg Ala Gln Pro
 110 115 120
 Ser Glu Lys Gln Cys Ala Arg Thr Leu Lys Asp Gln Ser Ser Glu
 125 130 135
 Phe Lys Ala Lys Ile Ile Phe Trp Tyr Val Leu Pro Ile Ser Ile
 140 145 150
 Thr Val Phe Leu Phe Ser Val Met Gly Tyr Ser Ile Tyr Arg Tyr
 155 160 165

Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile	170	175	180
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	185	190	195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	200	205	210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	215	220	225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	230	235	240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	245	250	255
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	260	265	270
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	275	280	285
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	290	295	300
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	305	310	315
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	320	325	330
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	335	340	345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	350	355	360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	365	370	375
Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser	380	385	390
Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Glu	Gly	395	400	405
Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro	410	415	420
Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly	425	430	435
Leu	Tyr	Val	Gln	Met	Glu	Asn									440		

<210> 105

<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct

<400> 105
cgctgctgct gttgctcctg g 21

<210> 106
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 106
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<210> 107
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 107
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<210> 108
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 108
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<210> 109
<211> 51
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

<222> 1-51
<223> Synthetic construct.

<400> 109
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<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

<400> 110
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tgaacggctc tgctgtcctg ggccctgcag tggggctgct gaggctgcca 500
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ctggggcttc gtgtctgact ttgaggagct gccgcctgga ctgatggagg 600
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cacctgacac ttaccatgct ctgcacccgc agtggggaca gccacagacg 700
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cccgacgtgt acacgcaggt gtccgccttt gtggcctgga tctgggacgt 850
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ccccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950
gccgctccag gcctggaatg ttccgtggct gggccccacg ggaagcctga 1000
tggttcagggg tgggggtggg cgggcagcgg tggggcacac ccattccaca 1050
tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val
1 5 10 15

Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp
20 25 30

Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg
35 40 45

Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly
50 55 60

Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys
65 70 75

Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala
80 85 90

His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile
95 100 105

Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala
110 115 120

Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly
125 130 135

Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro
140 145 150

Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val
155 160 165

Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val
170 175 180

Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His
185 190 195

Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg
200 205 210

Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg
215 220 225

Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly
230 235 240

Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val
245 250 255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
 260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
 275 280

<210> 112
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 112
 gacgtctgca acagctcctg gaag 24

<210> 113
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 113
 cgagaaggaa acgaggccgt gag 23

<210> 114
 <211> 44
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-44
 <223> Synthetic construct.

<400> 114
 tgacacttac catgctctgc acccgcagtg gggacagcca caga 44

<210> 115
 <211> 1808
 <212> DNA
 <213> Homo sapiens

<400> 115
 gagctaccca ggcggctggt gtgcagcaag ctccgcgccg actccggacg 50
 cctgacgcct gacgcctgtc cccggcccgg catgagccgc tacctgctgc 100
 cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150
 tatgtcaccg gtggggcttg cccagcaag gccaccatcc ctgggaagac 200

ggtcatcgtg acgggcgcca acacaggcat cgggaagcag accgccttgg 250
 aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300
 aagtgtgagg cggcagcaaa ggacatccgc ggggagacc tcaatcacca 350
 tgtcaacgcc cggcacctgg acttggttcc cctcaagtct atccgagagt 400
 ttgcagcaaa gatcattgaa gaggaggagc gagtggacat tctaataaac 450
 aacgcgggtg tgatgcggtg cccccactgg accaccgagg acggcttcga 500
 gatgcagttt ggcgttaacc acctgggtca ctttctcttg acaaacttgc 550
 tgctggacaa gctgaaagcc tcagcccctt cgcggatcat caacctctcg 600
 tccctggccc atgttgctgg gcacatagac tttgacgact tgaactggca 650
 gacgaggaag tataacacca aagccgccta ctgccagagc aagctcgcca 700
 tcgtcctctt caccaaggag ctgagccggc ggctgcaagg ctctggtgtg 750
 actgtcaacg ccctgcaccc cggcgtggcc aggacagagc tgggcagaca 800
 cacgggcata catggctcca cttctccag caccacactc gggcccatct 850
 tctggctgct ggtcaagagc cccgagctgg ccgccagcc cagcacatac 900
 ctggccgtgg cggaggaact ggcggatgtt tccggaaagt acttcgatgg 950
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 gtgagggagc agcccctccc cagataacct ctggagcaga tttgaaagcc 1100
 aggatggcgc ctccagaccg aggacagctg tccgccatgc ccgcagcttc 1150
 ctggcactac ctgagccggg agaccagga ctggcggccg ccatgcccgc 1200
 agtaggttct agggggcggt gctggccgca gtggactggc ctgcaggtga 1250
 gcaactgccc gggctctggc tggttccgtc tgcctctgct ccagcagggg 1300
 agaggggcca tctgatgctt cccctgggaa tctaaactgg gaatggccga 1350
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 gcctgtcggg gagggttcca aggtgctccg tgaagagcat gggcaagttg 1450
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 gctcattt 1808

<210> 116
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 116

Met	Ser	Arg	Tyr	Leu	Leu	Pro	Leu	Ser	Ala	Leu	Gly	Thr	Val	Ala	
1				5					10					15	
Gly	Ala	Ala	Val	Leu	Leu	Lys	Asp	Tyr	Val	Thr	Gly	Gly	Ala	Cys	
				20					25					30	
Pro	Ser	Lys	Ala	Thr	Ile	Pro	Gly	Lys	Thr	Val	Ile	Val	Thr	Gly	
				35					40					45	
Ala	Asn	Thr	Gly	Ile	Gly	Lys	Gln	Thr	Ala	Leu	Glu	Leu	Ala	Arg	
				50					55					60	
Arg	Gly	Gly	Asn	Ile	Ile	Leu	Ala	Cys	Arg	Asp	Met	Glu	Lys	Cys	
				65					70					75	
Glu	Ala	Ala	Ala	Lys	Asp	Ile	Arg	Gly	Glu	Thr	Leu	Asn	His	His	
				80					85					90	
Val	Asn	Ala	Arg	His	Leu	Asp	Leu	Ala	Ser	Leu	Lys	Ser	Ile	Arg	
				95					100					105	
Glu	Phe	Ala	Ala	Lys	Ile	Ile	Glu	Glu	Glu	Glu	Arg	Val	Asp	Ile	
				110					115					120	
Leu	Ile	Asn	Asn	Ala	Gly	Val	Met	Arg	Cys	Pro	His	Trp	Thr	Thr	
				125					130					135	
Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	Leu	Gly	His	
				140					145					150	
Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Asp	Lys	Leu	Lys	Ala	Ser	Ala	
				155					160					165	
Pro	Ser	Arg	Ile	Ile	Asn	Leu	Ser	Ser	Leu	Ala	His	Val	Ala	Gly	
				170					175					180	
His	Ile	Asp	Phe	Asp	Asp	Leu	Asn	Trp	Gln	Thr	Arg	Lys	Tyr	Asn	
				185					190					195	
Thr	Lys	Ala	Ala	Tyr	Cys	Gln	Ser	Lys	Leu	Ala	Ile	Val	Leu	Phe	
				200					205					210	
Thr	Lys	Glu	Leu	Ser	Arg	Arg	Leu	Gln	Gly	Ser	Gly	Val	Thr	Val	
				215					220					225	

Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
				230					235					240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
				320					325					330

Arg

<210> 117
 <211> 2249
 <212> DNA
 <213> Homo sapiens

<400> 117
 gaagttcgcg agcgctggca tgttgctcctg gggcgcggtt ggcggcgctg 50
 ctggcggtgc tggcgctcgg gacaggagac ccagaaaggg ctgcggctcg 100
 gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccc 150
 agcgccggct gctggggctg ctgaggcggg acctgcgcgg ggaggaggcg 200
 cggctgcggg acctgactag attctacgac aaggtacttt ctttgcata 250
 ggattcaaca acccctgtgg ctaaccctct gcttgcattt actctcatca 300
 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350
 gagaacatcc gagctctgaa ggatggctatgagaagggtg agcaagacct 400
 tccagccttt gaggaccttg agggagcagc aagggccctg atgcggctgc 450
 aggacgtgta catgctcaat gtgaaaggcc tggcccaggg tgtctttcag 500
 agagtcaactg gctctgccat cactgacctg tacagcccca aacggctctt 550
 ttctctcaca ggggatgact gcttccaagt tggcaagggt gcctatgaca 600
 tgggggatta ttaccatgcc attccatggc tggaggaggc tgcagtctc 650
 ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700

tacattatat aaggattttt ttttaagttga aaacaacttt cttttctttt 2200

tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
1 5 10 15

Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr
20 25 30

Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
35 40 45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
110 115 120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
185 190 195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
200 205 210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
215 220 225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
230 235 240

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Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu	245	250	255
Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr	260	265	270
Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala	275	280	285
Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr	290	295	300
Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr	305	310	315
Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala	320	325	330
Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu	335	340	345
Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala	350	355	360
Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val	365	370	375
Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser	380	385	390
Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr	395	400	405
Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro	410	415	420
Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly	425	430	435
His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro	440	445	450
Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile	455	460	465
Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr	470	475	480
Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp	485	490	495
Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His	500	505	510
Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys	515	520	525
Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser			

530

535

540

Ser Pro Glu Asp

<210> 119

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 119

cgggacagga gacccagaaa ggg 23

<210> 120

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 120

ggccaagtga tccaaggcat cttc 24

<210> 121

<211> 49

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-49

<223> Synthetic construct.

<400> 121

ctgcgggacc tgactagatt ctacgacaag gtactttcctt tgcattgggg 49

<210> 122

<211> 1778

<212> DNA

<213> Homo sapiens

<400> 122

gagataggga gtctggggtt aagttcctgc tccatctcag gagcccctgc 50

tcccaccctt aggaagccac cagactccac ggtgtggggc caatcaggtg 100

gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150

ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgccg 200

cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250
 gctcaagttt tcacttatca tctattccac cgtgttctgg ctgattgggg 300
 cctgggcct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350
 aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcatcctcct 400
 gggcgctcgtc atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450
 gtgacaacct gtaccttctc caagcattca tgtacatcct tgggatctgc 500
 ctcatcatgg agctcattgg tggcgtggtg gccttgacct tccggaacca 550
 gaccattgac ttctgaacy acaacattcg aagaggaatt gagaactact 600
 atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650
 aagtgtctgtg gcggggagga ctaccgagat tggagcaaga atcagtacca 700
 cgactgcagt gcccttgac cctggcctg tggggtgccc tacacctgct 750
 gcatcaggaa cagcagaaa gttgtcaaca ccatgtgtgg ctacaaaact 800
 atcgacaagg agcgtttcag tgtgcaggat gtcactctacg tgcggggctg 850
 caaccaagcc gtgatcatct ggttcatgga caactacacc atcatggcgt 900
 gcatcctcct gggcatcctg cttccccagt tcctgggggt gctgctgacg 950
 ctgctgtaca tcaccgggt ggaggacatc atcatggagc actctgtcac 1000
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 tccaacaagg accgtctggg atagcacctc tcagtcaaca tcgtggggct 1150
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 gctgtgtgtg cctgtgtgta ggtccacagg cctctgcctc ccaggggagc 1250
 agagcctggg cctcccctaa gaggttttcc ccgaggcagc tctggaatct 1300
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 ctacagggga gggagagcct gaggtctgct tcagggccca tttcatctct 1400
 ggcagtgcct tggcgtggtg attcaaggca gttttgtagc acctgtaatt 1450
 ggggagaggg agtgtgcccc tcggggcagg agggaagggc atctggggaa 1500
 gggcaggagg gaagagctgt ccatgcagcc acgcccattg ccaggttggc 1550
 ctcttctcag cctcccagggt gccttgagcc ctcttgcaag ggcggctgct 1600
 tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctgggtat ttccccgcac 1700
 gtcttattct tgcccttccc ccaaccagtt tgттаатcaa асаатааааа 1750
 catgttttgt tttgttttta аааааааа 1778

<210> 123
 <211> 294
 <212> PRT
 <213> Homo sapiens

<400> 123

Met	Pro	Arg	Gly	Asp	Ser	Glu	Gln	Val	Arg	Tyr	Cys	Ala	Arg	Phe	1	5	10	15
Ser	Tyr	Leu	Trp	Leu	Lys	Phe	Ser	Leu	Ile	Ile	Tyr	Ser	Thr	Val	20	25	30	
Phe	Trp	Leu	Ile	Gly	Ala	Leu	Val	Leu	Ser	Val	Gly	Ile	Tyr	Ala	35	40	45	
Glu	Val	Glu	Arg	Gln	Lys	Tyr	Lys	Thr	Leu	Glu	Ser	Ala	Phe	Leu	50	55	60	
Ala	Pro	Ala	Ile	Ile	Leu	Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Met	65	70	75	
Val	Ser	Phe	Ile	Gly	Val	Leu	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Tyr	80	85	90	
Leu	Leu	Gln	Ala	Phe	Met	Tyr	Ile	Leu	Gly	Ile	Cys	Leu	Ile	Met	95	100	105	
Glu	Leu	Ile	Gly	Gly	Val	Val	Ala	Leu	Thr	Phe	Arg	Asn	Gln	Thr	110	115	120	
Ile	Asp	Phe	Leu	Asn	Asp	Asn	Ile	Arg	Arg	Gly	Ile	Glu	Asn	Tyr	125	130	135	
Tyr	Asp	Asp	Leu	Asp	Phe	Lys	Asn	Ile	Met	Asp	Phe	Val	Gln	Lys	140	145	150	
Lys	Phe	Lys	Cys	Cys	Gly	Gly	Glu	Asp	Tyr	Arg	Asp	Trp	Ser	Lys	155	160	165	
Asn	Gln	Tyr	His	Asp	Cys	Ser	Ala	Pro	Gly	Pro	Leu	Ala	Cys	Gly	170	175	180	
Val	Pro	Tyr	Thr	Cys	Cys	Ile	Arg	Asn	Thr	Thr	Glu	Val	Val	Asn	185	190	195	
Thr	Met	Cys	Gly	Tyr	Lys	Thr	Ile	Asp	Lys	Glu	Arg	Phe	Ser	Val	200	205	210	
Gln	Asp	Val	Ile	Tyr	Val	Arg	Gly	Cys	Thr	Asn	Ala	Val	Ile	Ile	215	220	225	
Trp	Phe	Met	Asp	Asn	Tyr	Thr	Ile	Met	Ala	Cys	Ile	Leu	Leu	Gly				

230	235	240
Ile Leu Leu Pro Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu Tyr	
245	250	255
Ile Thr Arg Val Glu Asp Ile Ile Met	Glu His Ser Val Thr Asp	
260	265	270
Gly Leu Leu Gly Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala Gly	
275	280	285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn		
290		

<210> 124
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 124
 atcatctatt ccaccgtgtt ctggc 25

<210> 125
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 125
 gacagagtgc tccatgatga tgtcc 25

<210> 126
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 126
 cctgtctgtg ggcattctatg cagagggtga gcggcagaaa tataaaaccc 50

<210> 127
 <211> 1636
 <212> DNA
 <213> Homo sapiens

<400> 127

gaggagcggg ccgaggactc cagcgtgccc aggtotggca tcctgcactt 50
gctgccctct gacacctggg aagatggccg gcccggtggac cttcaccctt 100
ctctgtgggt tgctggcagc caccttgatc caagccaccc tcagtccac 150
tgcagtcttc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300
ggtgaacacc gtcctgaagc acatcatctg gctgaaggct atcacagcta 350
acatcctcca gctgcagggt aagccctcgg ccaatgacca ggagctgcta 400
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctgggtcaa 450
gaccatcgtg gaggttccaca tgacgactga ggccaagcc accatccgca 500
tggacaccag tgcaagtggc cccacccgcc tggtoctcag tgactgtgcc 550
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<210> 128
 <211> 484
 <212> PRT
 <213> Homo sapiens

<400> 128

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Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile	20	25	30	
Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys	35	40	45	
Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser	50	55	60	
Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser	65	70	75	
Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile	80	85	90	
Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp	95	100	105	
Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe	110	115	120	
Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr	125	130	135	
Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro	140	145	150	
Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu	155	160	165	
Arg	Ile	Gln	Leu	Leu	Tyr	Lys	Leu	Ser	Phe	Leu	Val	Asn	Ala	Leu	170	175	180	
Ala	Lys	Gln	Val	Met	Asn	Leu	Leu	Val	Pro	Ser	Leu	Pro	Asn	Leu	185	190	195	
Val	Lys	Asn	Gln	Leu	Cys	Pro	Val	Ile	Glu	Ala	Ser	Phe	Asn	Gly	200	205	210	
Met	Tyr	Ala	Asp	Leu	Leu	Gln	Leu	Val	Lys	Val	Pro	Ile	Ser	Leu	215	220	225	

Ser	Ile	Asp	Arg	Leu	Glu	Phe	Asp	Leu	Leu	Tyr	Pro	Ala	Ile	Lys	
				230					235					240	
Gly	Asp	Thr	Ile	Gln	Leu	Tyr	Leu	Gly	Ala	Lys	Leu	Leu	Asp	Ser	
				245					250					255	
Gln	Gly	Lys	Val	Thr	Lys	Trp	Phe	Asn	Asn	Ser	Ala	Ala	Ser	Leu	
				260					265					270	
Thr	Met	Pro	Thr	Leu	Asp	Asn	Ile	Pro	Phe	Ser	Leu	Ile	Val	Ser	
				275					280					285	
Gln	Asp	Val	Val	Lys	Ala	Ala	Val	Ala	Ala	Val	Leu	Ser	Pro	Glu	
				290					295					300	
Glu	Phe	Met	Val	Leu	Leu	Asp	Ser	Val	Leu	Pro	Glu	Ser	Ala	His	
				305					310					315	
Arg	Leu	Lys	Ser	Ser	Ile	Gly	Leu	Ile	Asn	Glu	Lys	Ala	Ala	Asp	
				320					325					330	
Lys	Leu	Gly	Ser	Thr	Gln	Ile	Val	Lys	Ile	Leu	Thr	Gln	Asp	Thr	
				335					340					345	
Pro	Glu	Phe	Phe	Ile	Asp	Gln	Gly	His	Ala	Lys	Val	Ala	Gln	Leu	
				350					355					360	
Ile	Val	Leu	Glu	Val	Phe	Pro	Ser	Ser	Glu	Ala	Leu	Arg	Pro	Leu	
				365					370					375	
Phe	Thr	Leu	Gly	Ile	Glu	Ala	Ser	Ser	Glu	Ala	Gln	Phe	Tyr	Thr	
				380					385					390	
Lys	Gly	Asp	Gln	Leu	Ile	Leu	Asn	Leu	Asn	Asn	Ile	Ser	Ser	Asp	
				395					400					405	
Arg	Ile	Gln	Leu	Met	Asn	Ser	Gly	Ile	Gly	Trp	Phe	Gln	Pro	Asp	
				410					415					420	
Val	Leu	Lys	Asn	Ile	Ile	Thr	Glu	Ile	Ile	His	Ser	Ile	Leu	Leu	
				425					430					435	
Pro	Asn	Gln	Asn	Gly	Lys	Leu	Arg	Ser	Gly	Val	Pro	Val	Ser	Leu	
				440					445					450	
Val	Lys	Ala	Leu	Gly	Phe	Glu	Ala	Ala	Glu	Ser	Ser	Leu	Thr	Lys	
				455					460					465	
Asp	Ala	Leu	Val	Leu	Thr	Pro	Ala	Ser	Leu	Trp	Lys	Pro	Ser	Ser	
				470					475					480	
Pro	Val	Ser	Gln												

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

<400> 129

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ctaacaaaag acctgtaata agaataatg gagacaagtt ccgtgcctt 200
gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcaactgctct 250
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agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350
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atctggtcaa atgtggaacc atataagagg accaccatat gcccataaga 750
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ctttctgatg agttaaaaag gtcccagaga tatatagaca ctggagtact 1050
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 gaacaccatt cttcagagca cacgtctagc cctcagcaag acagttgttt 1600
 ctctctctcc ttgcatatct cctactgctc tccagcctga gtgatagagt 1650
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 gcttgagtat ggtgttaact acctgtatt tagaaagatt tcagattcat 1750
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 aaattagagt ttgtcactta ttccatttgt acctaagaga aaaataggct 1900
 cagttagaaa aggactccct ggccaggcgc agtgacttac gcctgtaate 1950
 tcagcacttt gggaggccaa ggcaggcaga tcacgaggtc aggagttcga 2000
 gaccatcctg gccaacatgg tgaaaccccg tctctactaa aaatataaaa 2050
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 aaaaaaaaaa aaa 2213

<210> 130

<211> 335

<212> PRT

<213> Homo sapiens

<400> 130

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Val	Ala	Leu	Leu	Ile	Val	Cys	Asp	Val	Pro	Ser	Ala	Ser	Ala	Gln
				20					25					30
Arg	Lys	Lys	Glu	Met	Val	Leu	Ser	Glu	Lys	Val	Ser	Gln	Leu	Met
				35					40					45
Glu	Trp	Thr	Asn	Lys	Arg	Pro	Val	Ile	Arg	Met	Asn	Gly	Asp	Lys
				50					55					60
Phe	Arg	Arg	Leu	Val	Lys	Ala	Pro	Pro	Arg	Asn	Tyr	Ser	Val	Ile
				65					70					75
Val	Met	Phe	Thr	Ala	Leu	Gln	Leu	His	Arg	Gln	Cys	Val	Val	Cys
				80					85					90
Lys	Gln	Ala	Asp	Glu	Glu	Phe	Gln	Ile	Leu	Ala	Asn	Ser	Trp	Arg
				95					100					105

Tyr	Ser	Ser	Ala	Phe	Thr	Asn	Arg	Ile	Phe	Phe	Ala	Met	Val	Asp	
				110					115					120	
Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser	
				125					130					135	
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg	
				140					145					150	
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln	
				155					160					165	
Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val	
				170					175					180	
Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu	
				185					190					195	
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met	
				200					205					210	
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys	
				215					220					225	
Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg	
				230					235					240	
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn	
				245					250					255	
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His	
				260					265					270	
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu	
				275					280					285	
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys	
				290					295					300	
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser	
				305					310					315	
Trp	Met	Leu	Ser	Ile	Phe	Arg	Ser	Lys	Tyr	His	Gly	Tyr	Pro	Tyr	
				320					325					330	
Ser	Phe	Leu	Met	Ser											
				335											

<210> 131

<211> 2476

<212> DNA

<213> Homo sapiens

<400> 131

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 cagccaaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250
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 cctattcgga tggatcatca atattgcctc aactcttga tctttcctcg 1450
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 ttctttggat cagaagcttc attccattat aaactaccct aaagtttctg 1550

Asn Ser Pro Ile Cys Cys Pro Ser Arg Ala Ala Met Trp Ser Gly	80	85	90
Leu Phe Thr His Leu Thr Glu Ser Trp Asn Asn Phe Lys Gly Leu	95	100	105
Asp Pro Asn Tyr Thr Thr Trp Met Asp Val Met Glu Arg His Gly	110	115	120
Tyr Arg Thr Gln Lys Phe Gly Lys Leu Asp Tyr Thr Ser Gly His	125	130	135
His Ser Ile Ser Asn Arg Val Glu Ala Trp Thr Arg Asp Val Ala	140	145	150
Phe Leu Leu Arg Gln Glu Gly Arg Pro Met Val Asn Leu Ile Arg	155	160	165
Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp Trp Gln Asn Thr	170	175	180
Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile Asn Tyr Thr	185	190	195
Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His Pro Tyr	200	205	210
Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe His	215	220	225
Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys	230	235	240
Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr	245	250	255
Tyr Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys	260	265	270
Glu Ile Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu	275	280	285
Thr Asp Ala Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu	290	295	300
Asp Leu Leu Gln Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly	305	310	315
Glu Leu Ala Met Glu His Arg Gln Phe Tyr Lys Met Ser Met Tyr	320	325	330
Glu Ala Ser Ala His Val Pro Leu Leu Met Met Gly Pro Gly Ile	335	340	345
Lys Ala Gly Leu Gln Val Ser Asn Val Val Ser Leu Val Asp Ile	350	355	360
Tyr Pro Thr Met Leu Asp Ile Ala Gly Ile Pro Leu Pro Gln Asn			

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	365	370	375
Leu Ser Gly Tyr	Ser Leu Leu Pro Leu	Ser Ser Glu Thr Phe	Lys
	380	385	390
Asn Glu His Lys	Val Lys Asn Leu His	Pro Pro Trp Ile Leu	Ser
	395	400	405
Glu Phe His Gly	Cys Asn Val Asn Ala	Ser Thr Tyr Met Leu	Arg
	410	415	420
Thr Asn His Trp	Lys Tyr Ile Ala Tyr	Ser Asp Gly Ala Ser	Ile
	425	430	435
Leu Pro Gln Leu	Phe Asp Leu Ser Ser	Asp Pro Asp Glu Leu	Thr
	440	445	450
Asn Val Ala Val	Lys Phe Pro Glu Ile	Thr Tyr Ser Leu Asp	Gln
	455	460	465
Lys Leu His Ser	Ile Ile Asn Tyr Pro	Lys Val Ser Ala Ser	Val
	470	475	480
His Gln Tyr Asn	Lys Glu Gln Phe Ile	Lys Trp Lys Gln Ser	Ile
	485	490	495
Gly Gln Asn Tyr	Ser Asn Val Ile Ala	Asn Leu Arg Trp His	Gln
	500	505	510
Asp Trp Gln Lys	Glu Pro Arg Lys Tyr	Glu Asn Ala Ile Asp	Gln
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Trp Leu Lys Thr	His Met Asn Pro Arg	Ala Val	
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<211> 1475
<212> DNA
<213> Homo sapiens

<400> 133
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ctacatccta ggccttctgg ggcttttggg cacaactggtt gccatgctgc 200
tcccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250
gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300
catcaccag tgtgacatct atagaccct tctgggcctg cccgctgaca 350
tccaggctgc ccaggccatg atggtgacat ccagtgaat ctctccctg 400
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atcccagagcc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500
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 gtgaaaaaca gtggacagca ccccgagggc cacaggtgag ggacactacc 900
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 attgccaaagg atgctcgcca tgccagcctt tctgttttcc tcaccttgct 1050
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 ccccaaacct actaatcaca tccactgac tgaccctctg tgatcaaaga 1200
 ccctctctct ggctgagggt ggctcttagc tcattgctgg ggatgggaag 1250
 gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc 1300
 cctccaaaga aactgattgg ccctggaacc tccatccac tcttgttatg 1350
 actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc 1400
 tacggtatcc agggaacaga aagcaggatg caggatggga ggacaggaag 1450
 gcagcctggg acatttaaaa aaata 1475

<210> 134

<211> 230

<212> PRT

<213> Homo sapiens

<400> 134

Met	Ala	Ser	Leu	Gly	Leu	Gln	Leu	Val	Gly	Tyr	Ile	Leu	Gly	Leu
1				5					10					15

Leu	Gly	Leu	Leu	Gly	Thr	Leu	Val	Ala	Met	Leu	Leu	Pro	Ser	Trp
				20					25					30

Lys	Thr	Ser	Ser	Tyr	Val	Gly	Ala	Ser	Ile	Val	Thr	Ala	Val	Gly
				35					40					45

Phe	Ser	Lys	Gly	Leu	Trp	Met	Glu	Cys	Ala	Thr	His	Ser	Thr	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50					55					60				
Ile	Thr	Gln	Cys	Asp	Ile	Tyr	Ser	Thr	Leu	Leu	Gly	Leu	Pro	Ala
				65					70					75
Asp	Ile	Gln	Ala	Ala	Gln	Ala	Met	Met	Val	Thr	Ser	Ser	Ala	Ile
				80					85					90
Ser	Ser	Leu	Ala	Cys	Ile	Ile	Ser	Val	Val	Gly	Met	Arg	Cys	Thr
				95					100					105
Val	Phe	Cys	Gln	Glu	Ser	Arg	Ala	Lys	Asp	Arg	Val	Ala	Val	Ala
				110					115					120
Gly	Gly	Val	Phe	Phe	Ile	Leu	Gly	Gly	Leu	Leu	Gly	Phe	Ile	Pro
				125					130					135
Val	Ala	Trp	Asn	Leu	His	Gly	Ile	Leu	Arg	Asp	Phe	Tyr	Ser	Pro
				140					145					150
Leu	Val	Pro	Asp	Ser	Met	Lys	Phe	Glu	Ile	Gly	Glu	Ala	Leu	Tyr
				155					160					165
Leu	Gly	Ile	Ile	Ser	Ser	Leu	Phe	Ser	Leu	Ile	Ala	Gly	Ile	Ile
				170					175					180
Leu	Cys	Phe	Ser	Cys	Ser	Ser	Gln	Arg	Asn	Arg	Ser	Asn	Tyr	Tyr
				185					190					195
Asp	Ala	Tyr	Gln	Ala	Gln	Pro	Leu	Ala	Thr	Arg	Ser	Ser	Pro	Arg
				200					205					210
Pro	Gly	Gln	Pro	Pro	Lys	Val	Lys	Ser	Glu	Phe	Asn	Ser	Tyr	Ser
				215					220					225
Leu	Thr	Gly	Tyr	Val										
				230										

<210> 135
 <211> 610
 <212> DNA
 <213> Homo sapiens

<400> 135
 gcactgctgc tgtcccatca gctgctctga agtccatgg tgcccagaat 50
 ctctgctcct gcttatgtgt cagtctgtct cctcctcttg tgtccaagg 100
 aagtcacgc tcccgtggc tcagaacct ggctgtgcca gccggcacc 150
 aggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200
 cgccatcgtg tccctgagcg agaccgcca atgtgggtccc cctgcacct 250
 tctggccctg ctttgagctc tgctgtcttg attcctttgg cctcacaac 300
 gattttgttg tgaagctgaa ggttcagggt gtgaattccc agtgccactc 350

atctcccatc tccagtaa at gtgaaagcag aagacgtttt ccctgagaag 400
 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
 atgacagtag attatcagga aataaataaa gtgggtttttc caatgtacac 600
 acctgtaaaa 610

<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
 1 5 10 15
 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
 65 70 75
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
 80 85 90
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
 95 100 105
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
 110 115

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
 ctccactgca accaccaga gccatggctc cccgaggctg catcgtagct 50
 gtcttttgcca ttttctgcat ctccaggctc ctctgctcac acggagcccc 100
 agtggtcccc atgactcctt acctgatgct gtgccagcca cacaagagat 150
 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200
 gtctgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

ctgctttgag cagtgtgcc cctggacctt catggtgaag ctgataaacc 300
 agaactgcga ctacgcccgg acctcggatg acaggctttg tcgcagtgtc 350
 agctaattga acatcagggg aacgatgact cctggattct ccttcctggg 400
 tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagtg 450
 gctgttttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500
 gacctgtctg aggcccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550
 ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600
 ggactctgaa cctcctgat gaccctatg gccaacatca acccggcacc 650
 accccaaggc tggctgggga acccttcacc cttctgtgag attttccatc 700
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 tatgtacttt ataatgaaa a 771

<210> 138

<211> 110

<212> PRT

<213> Homo sapiens

<400> 138

Met	Ala	Pro	Arg	Gly	Cys	Ile	Val	Ala	Val	Phe	Ala	Ile	Phe	Cys	1	5	10	15
Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met	20	25	30	
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp	35	40	45	
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val	50	55	60	
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg	65	70	75	
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu	80	85	90	
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu	95	100	105	
Cys	Arg	Ser	Val	Ser											110			

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

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 ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggctc 150
 cccacggccc tggaggccgg cagctggcgc tggggatccc tgctcttcgc 200
 tctcttctctg gctgcgtccc taggtccggt ggcagccttc aaggctcgca 250
 cgccgtatcc cctgtatgtc tgtcccagg ggcagaacgt caccctcacc 300
 tgcaggctct tgggccctgt ggacaaaggg cagcatgtga cttctacaa 350
 gacgtggtac cgcagctcga ggggcgaggt gcagacctgc tcagagcgcc 400
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 caccactcgg agcacagggt ccatggtgcc atggagctgc aggtgcagac 650
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<210> 140

<211> 311

<212> PRT

<213> Homo sapiens

<400> 140

Met	Gly	Val	Pro	Thr	Ala	Leu	Glu	Ala	Gly	Ser	Trp	Arg	Trp	Gly	1	5	10	15
Ser	Leu	Leu	Phe	Ala	Leu	Phe	Leu	Ala	Ala	Ser	Leu	Gly	Pro	Val	20	25	30	
Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro	35	40	45	
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val	50	55	60	
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser	65	70	75	
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg	80	85	90	
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln	95	100	105	
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu	110	115	120	
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn	125	130	135	
Leu	Thr	Leu	Leu	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Glu				

140 145 150
 Ile Arg His His His Ser Glu His Arg Val His Gly Ala Met Glu
 155 160 165
 Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val
 170 175 180
 Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr Ala Ala Ala
 185 190 195
 Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu
 200 205 210
 Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg
 215 220 225
 Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile
 230 235 240
 Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro
 245 250 255
 Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln
 260 265 270
 Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro
 275 280 285
 Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp
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 Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile
 305 310

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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<210> 142
<211> 451
<212> PRT
<213> Homo sapiens

<400> 142

Met	Val	Pro	Glu	Val	Arg	Val	Leu	Ser	Ser	Leu	Leu	Gly	Leu	Ala	1	5	10	15
Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp	20	25	30	
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser	35	40	45	
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg	50	55	60	
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His	65	70	75	
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln	80	85	90	
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg	95	100	105	
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His	110	115	120	
Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	125	130	135	
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	140	145	150	
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	155	160	165	
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	170	175	180	
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	185	190	195	
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	200	205	210	
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	215	220	225	
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	230	235	240	
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	245	250	255	
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	260	265	270	
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	275	280	285	
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys				

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290	295	300
Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro		
305	310	315
Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg		
320	325	330
Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser		
335	340	345
Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala		
350	355	360
Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu		
365	370	375
Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His		
380	385	390
Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala		
395	400	405
Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro		
410	415	420
Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala		
425	430	435
Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys		
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Thr		

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 <211> 693
 <212> DNA
 <213> Homo sapiens

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 cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150
 tgggctacgc gctcctcggt atcgtgaccc cgggagagcg gcggaagcag 200
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250
 ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300
 cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350
 ggcgccagcg ggaggtcacc gtgagaccgg acttgccctcc gtgggcgccg 400
 gaccttggtt tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450

ccagcggaga gtccggaccg agataccatg ccaggactct ccggggctcct 500
 gtgagctgcc gtccgggtgag cacgtttccc ccaaaccctg gactgactgc 550
 ttttaagggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 144
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 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
 35 40 45
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
 50 55 60
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
 65 70 75
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
 80 85 90
 Arg Ser Pro

<210> 145
 <211> 1883
 <212> DNA
 <213> Homo sapiens

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 caggctgcca tggggcccag caccctctc ctcatottgt tccttttgtc 150
 atggtcggga cccctccaag gacagcagca ccaccttggt gagtacatgg 200
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300
 actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350
 acaccatctc cgggagagtg gatcgtcttg agcgggaggt agactatctg 400

gagacccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450
tgagggccct gggaccaaag gcaaggggaag aaggaatgag aagtacgata 500
tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550
ctgaagcgat ttggtggccc agctggtcta tggaccaagg atccactggg 600
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ttgtcttccc aaggctgcgt gacttcaccc ttgccatggc tgcccggaaa 700
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cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950
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<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

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Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
			20						25					30
Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
			35						40					45
Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
			50						55					60
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala
			65						70					75
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu
			80						85					90
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro
			95						100					105
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys
			110						115					120
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys
			125						130					135
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg
			140						145					150
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln
			155						160					165
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala
			170						175					180
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala
			185						190					195
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr
			200						205					210
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro
			215						220					225
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln
			230						235					240
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser
			245						250					255

Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala	
				260					265					270	
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala	
				275					280					285	
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys	
				290					295					300	
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro	
				305					310					315	
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr	
				320					325					330	
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile	
				335					340					345	
Gln	Cys	Ser	Phe	Asp	Ala	Ser	Gly	Thr	Leu	Thr	Pro	Glu	Arg	Ala	
				350					355					360	
Ala	Leu	Pro	Tyr	Phe	Pro	Arg	Arg	Tyr	Gly	Ala	His	Ala	Ser	Leu	
				365					370					375	
Arg	Tyr	Asn	Pro	Arg	Glu	Arg	Gln	Leu	Tyr	Ala	Trp	Asp	Asp	Gly	
				380					385					390	
Tyr	Gln	Ile	Val	Tyr	Lys	Leu	Glu	Met	Arg	Lys	Lys	Glu	Glu	Glu	
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<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

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 aaaactgtaa cccatagaaa agctcccag gaggtgcctc actctgagaa 1150
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 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350
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 ccacctctca ggtgaagaac cgtcaggaat tccatctca caggctgtgg 1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000
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aa 2052

<210> 148
<211> 500
<212> PRT
<213> Homo sapiens

<400> 148

Met	Ala	Leu	Met	Leu	Ser	Leu	Val	Leu	Ser	Leu	Leu	Lys	Leu	Gly	1	5	10	15
Ser	Gly	Gln	Trp	Gln	Val	Phe	Gly	Pro	Asp	Lys	Pro	Val	Gln	Ala	20	25	30	
Leu	Val	Gly	Glu	Asp	Ala	Ala	Phe	Ser	Cys	Phe	Leu	Ser	Pro	Lys	35	40	45	
Thr	Asn	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Gly	Gln	Phe	50	55	60	
Ser	Ser	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Lys	Asp	Gln	Pro	Phe	65	70	75	
Met	Gln	Met	Pro	Gln	Tyr	Gln	Gly	Arg	Thr	Lys	Leu	Val	Lys	Asp	80	85	90	
Ser	Ile	Ala	Glu	Gly	Arg	Ile	Ser	Leu	Arg	Leu	Glu	Asn	Ile	Thr	95	100	105	
Val	Leu	Asp	Ala	Gly	Leu	Tyr	Gly	Cys	Arg	Ile	Ser	Ser	Gln	Ser	110	115	120	
Tyr	Tyr	Gln	Lys	Ala	Ile	Trp	Glu	Leu	Gln	Val	Ser	Ala	Leu	Gly	125	130	135	
Ser	Val	Pro	Leu	Ile	Ser	Ile	Thr	Gly	Tyr	Val	Asp	Arg	Asp	Ile	140	145	150	
Gln	Leu	Leu	Cys	Gln	Ser	Ser	Gly	Trp	Phe	Pro	Arg	Pro	Thr	Ala	155	160	165	
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Thr	Asp	Ser	Arg	170	175	180	
Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu	Ile	Ser	Leu	185	190	195	
Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met	Arg	His	200	205	210	
Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly	Asp	215	220	225	
Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	His	Leu	Ala	Thr	Lys	Val	Leu				

230	235	240
Gly Ile Leu Cys Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu Lys	
245	250	255
Ile Phe Phe Ser Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp	
260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu	Leu Arg Asp Ala Arg Lys	
275	280	285
His Ala Val Glu Val Thr Leu Asp Pro	Glu Thr Ala His Pro Lys	
290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro	
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val	
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val	
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr	
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr	
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg	
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn	
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu	
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu	
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu	
485	490	495
Pro Arg Gly Glu Met		
500		

<210> 149

<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gcgtggtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
ggaactgacc cagtgtgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgcc cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
gcgatggtgc gcccggtggc ggtggcggcg gcggttgccg aggtttcctt 50
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150
gcctcgccct gttgtgctgc gccgccgccg ccgccgccgt cgcctcagcc 200
gcctcggcgg ggaatgtcac cgttggcggc ggggccgcgg ggcaggtgga 250
cgcgctgccg ggccccgggt tgcggggcga gccagccac cccttccta 300
gggcgacggc tcccacggcc caggccccga ggaccgggcc cccgcgcgcc 350
accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400

caccctctt tgggcgactg ctggaccctc ttccaccacc tttcaggcgc 450
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 aaaaggctgc tactctcaag gaccatactg gtttaaacaa aggaggatga 1000
 gggcataga tttaaaaaat attttatata cttttattct cttactttat 1050
 atgttatatt taatgtcagg atttaaaaac atctaattta ctgatttagt 1100
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 agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Ileu	Ala	Leu	Leu	Cys	Cys	1	5	10	15
Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn	20	25	30	
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro	35	40	45	
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala	50	55	60	
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala	65	70	75	
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro	80	85	90	
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr	95	100	105	
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala	110	115	120	
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro	125	130	135	
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val	140	145	150	
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro	155	160	165	
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro				

	170		175		180
Ala Thr Glu Ala	Pro Ser Ser Pro Pro	Pro Glu Tyr Val Cys Asn			
	185	190			195
Cys Ser Val Val	Gly Ser Leu Asn Val	Asn Arg Cys Asn Gln Thr			
	200	205			210
Thr Gly Gln Cys	Glu Cys Arg Pro Gly	Tyr Gln Gly Leu His Cys			
	215	220			225
Glu Thr Cys Lys	Glu Gly Phe Tyr Leu	Asn Tyr Thr Ser Gly Leu			
	230	235			240
Cys Gln Pro Cys	Asp Cys Ser Pro His	Gly Ala Leu Ser Ile Pro			
	245	250			255

Cys Asn Arg

<210> 154
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 154
 aactgctctg tgggtggaag cctg 24

<210> 155
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 155
 cagtcacatg gctgacagac ccac 24

<210> 156
 <211> 38
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-38
 <223> Synthetic construct.

<400> 156
 aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157
 <211> 689
 <212> DNA
 <213> Homo sapiens

<400> 157
 tgcggcgcag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50
 ttctggcttt ggtctcggtg cccagggccc aggccgtgtg gttgggaaga 100
 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150
 ccgggaaaag ggctttgcc a tgagaagga catgaagaac gtcgtggggg 200
 tgggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250
 cacgggcttg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300
 ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350
 tgctggccac caacttcaga gactatgcc a tcattctcac tcagctggag 400
 ttccggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
 agccagccag gagggccatgg ggctcttcac caagtggagc aggagcctgg 500
 gcttcctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgccaca 600
 gggctcctgtg acctgggcca gtgtccacc acctcgctca gcggctcccg 650
 gggccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 158
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
 1 5 10 15
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
 20 25 30
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35 40 45
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50 55 60
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65 70 75
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80 85 90

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
			95						100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
			110						115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
			125						130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
			140						145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
			155						160					

<210> 159

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 159

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gtaaactgct gacgatgcag agttccgtga cgggtgcagga aggcctgtgt 150
gtccatgtgc cctgctcctt ctccctacccc tcgcatggct ggatttaccc 200
tggcccagta gttcatggct actggttccg ggaagggggcc aatacagacc 250
aggatgctcc agtggccaca aacaaccag ctcgggcagt gtgggaggag 300
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
cctgagcatc agagatgcc aagaagtga tgcggggaga tacttctttc 400
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
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tggctctgtg agttgatgca gttgacagca atccccctgc caggctgagc 900
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 acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctcagggggcc 1250
 cctgactgaa cttggggcag aagacagtcc cccagaccag cctccccccag 1300
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 acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala	1	5	10	15
Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr	20	25	30	
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr	35	40	45	
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr	50	55	60	
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala	65	70	75	
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg	80	85	90	
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser	95	100	105	
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg				

110	115	120
Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu		
125	130	135
Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile		
140	145	150
Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser		
155	160	165
Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp		
170	175	180
Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser		
185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser		
200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn		
215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr		
230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly		
245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu		
260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu		
275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser		
290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala		
305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln		
320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val		
335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe		
350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys		
365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu		
380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr		
395	400	405

Glu	Pro	Trp	Ala	Glu	Asp	Ser	Pro	Pro	Asp	Gln	Pro	Pro	Pro	Ala
				410					415					420
Ser	Ala	Arg	Ser	Ser	Val	Gly	Glu	Gly	Glu	Leu	Gln	Tyr	Ala	Ser
				425					430					435
Leu	Ser	Phe	Gln	Met	Val	Lys	Pro	Trp	Asp	Ser	Arg	Gly	Gln	Glu
				440					445					450
Ala	Thr	Asp	Thr	Glu	Tyr	Ser	Glu	Ile	Lys	Ile	His	Arg		
				455					460					

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
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 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150
 tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagt 200
 aaggtgacag ccctgggcgg tgggaagttg gaagccacgt tcaccttcat 250
 gagggaggat cggatcatcc agaagaaaat cctgatgcgg aagacggagg 300
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
 gagctgcca ggagggacca ctacatcttt tactgcaaag accagcacca 400
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
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 gctcccaccc acctgactcc aaataaagtc cttttcccc aaaaaaaaaa 700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
 1 5 10 15
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20	25	30
Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg		
35	40	45
Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly		
50	55	60
Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile		
65	70	75
Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu Pro Gly Lys Tyr		
80	85	90
Ser Ala Tyr Gly Gly Arg Lys Leu Met Tyr Leu Gln Glu Leu Pro		
95	100	105
Arg Arg Asp His Tyr Ile Phe Tyr Cys Lys Asp Gln His His Gly		
110	115	120
Gly Leu Leu His Met Gly Lys Leu Val Gly Arg Asn Ser Asp Thr		
125	130	135
Asn Arg Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln Arg Lys		
140	145	150
Gly Leu Ser Glu Glu Asp Ile Phe Thr Pro Leu Gln Thr Gly Ser		
155	160	165
Cys Val Pro Glu His		
170		

<210> 163

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-22

<223> Synthetic construct.

<400> 163

ggagatgaag accctgttcc tg 22

<210> 164

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 164

ggagatgaag accctgttcc tgggtg 26

<210> 165
<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct.

<400> 165
gtcctccgga aagtccttat c 21

<210> 166
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 166
gcctagtgtt cgggaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 167
cagggacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 168
ctgtccttca ccctggagga ggaggatata acagggacct ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169

gttccgcaga tgcagagggt gaggtggctg cgggactgga agtcatcggg 50
 cagagggtctc acagcagcca aggaacctgg gggccgctcc tccccctcc 100
 agggcatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150
 gtagggggag agaccaggat catcaagggg ttcgagtgc agcctcactc 200
 ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtggg 250
 cgacgctcat cggccccaga tggtcctga cagcagccca ctgcctcaag 300
 ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350
 ctgtgagcag acccgacag ccaactgagtc cttccccac cccggcttca 400
 acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450
 atggcatcgc cagtctccat cacctgggt gtgcgacccc tcacctctc 500
 ctacgctgt gtcactgctg gcaccagctg cctcatttcc ggctggggca 550
 gcacgtccag cccccagtta cgctgcctc acaccttgcg atgcgccaac 600
 atcaccatca ttgagcacca gaagtgtgag aacgcctacc cgggaacat 650
 cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
 gccaggggtga ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750
 attatctcct ggggccagga tccgtgtgag atcacccgaa agcctggtgt 800
 ctacacgaaa gtctgcaaat atgtggactg gatccaggag acgatgaaga 850
 acaattagac tggaccacc caccacagcc catcacctc cattccact 900
 tgggtgtttg ttctgttca ctctgttaat aagaaacct aagccaagac 950
 cctctacgaa cattctttg gcctcctgga ctacaggaga tgctgtcact 1000
 taataatcaa cctgggggtc gaaatcagt agacctgat tcaaattctg 1050
 ccttgaaata ttgtgactct gggaatgaca acacctggtt tgttctctgt 1100
 tgtatcccca gcccacaa cagctcctgg ccatatatca aggtttcaat 1150
 aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
 aaaa 1204

<210> 170

<211> 250

<212> PRT

<213> Homo sapiens

<400> 170

Met	Arg	Ile	Leu	Gln	Leu	Ile	Leu	Leu	Ala	Leu	Ala	Thr	Gly	Leu
1				5					10					15

Val	Gly	Gly	Glu	Thr	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro	20	25	30
His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu	35	40	45
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala	50	55	60
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His	65	70	75
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr	80	85	90
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys	95	100	105
Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val	110	115	120
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys	125	130	135
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr	140	145	150
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn	155	160	165
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly	170	175	180
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly	185	190	195
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	200	205	210
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	215	220	225
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	230	235	240
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						245	250	

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 171
ggctgcggga ctggaagtca tcggg 25

<210> 172
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 172
ctccaggcca tgaggattct gcag 24

<210> 173
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 173
cctctggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 174
tctgtgatgt tgcgggggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 175
cgtgtagaca ccaggctttc ggggtg 25

<210> 176
<211> 18
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctgggc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggcctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttogagt gcaagcctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc ttttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaaa atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaagg agacctacta aatgcccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atggtttggtt cttgggtgttg ggcaagtc 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450
 tgtgaccaa ggaccacgga gcattgagac atttaaaca atagacatgg 500
 acaatgacag gcagctctct aaagccgaga taaacctota cttgcaaagg 550
 gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600
 tttagaagat atttttaaga agaatgacca tgatgggtgat ggcttcattt 650
 ctccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700
 atttctactt ttttttttta gctatttact gtactttatg tataaaacaa 750
 agtcactttt ctccaagttg tatttgctat ttttcccta tgagaagata 800
 ttttgatctc cccaatacat tgattttggt ataataaatg tgaggctggt 850
 ttgcaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
 aaaaaaa 907

<210> 180
 <211> 222
 <212> PRT
 <213> Homo sapiens

<400> 180
 Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe
 1 5 10 15
 Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu
 20 25 30
 Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn
 35 40 45
 Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr
 50 55 60
 Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg
 65 70 75
 Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly
 80 85 90
 Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro
 95 100 105
 Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly
 110 115 120
 Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu
 125 130 135
 Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser
 140 145 150

Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu
				155					160					165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys
				170					175					180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu
				185					190					195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser
				200					205					210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu			
				215					220					

<210> 181
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 181
 gtgtttctgct ggagccgatg cc 22

<210> 182
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 182
 gacatggaca atgacagg 18

<210> 183
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 183
 cctttcagga tgtaggag 18

<210> 184
 <211> 18
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 184
gatgtctgcc accccaag 18

<210> 185
<211> 27
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-27
<223> Synthetic construct.

<400> 185
gcacacctgat atgacttgct acgtggc 27

<210> 186
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 186
tacaagaggg aagaggagtt gcac 24

<210> 187
<211> 52
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-52
<223> Synthetic construct.

<400> 187
gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50
cc 52

<210> 188
<211> 573
<212> DNA
<213> Homo sapiens

<400> 188
cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50
ctctttggag ctgtgactca gaaaaccaa acttctctgtg ctaagtgcc 100

cccaaatgct tcctgtgtca ataacactca ctgcacctgc aacctggat 150
 atactttctgg atctgggcag aaactattca cattccccctt ggagacatgt 200
 aacgccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250
 aaggcagggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300
 atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350
 ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400
 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450
 ctccagcatg gatgacagag caagactcgg tctcaaaaag aaaagatagt 500
 ttcttgtttc atttcgagac tgccctctca gtgtttcctg ggatccccctc 550
 ccaaataaag tacttatatt etc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

Met	Gln	Gly	Pro	Leu	Leu	Leu	Pro	Gly	Leu	Cys	Phe	Leu	Leu	Ser
1				5					10					15
Leu	Phe	Gly	Ala	Val	Thr	Gln	Lys	Thr	Lys	Thr	Ser	Cys	Ala	Lys
				20					25					30
Cys	Pro	Pro	Asn	Ala	Ser	Cys	Val	Asn	Asn	Thr	His	Cys	Thr	Cys
				35					40					45
Asn	His	Gly	Tyr	Thr	Ser	Gly	Ser	Gly	Gln	Lys	Leu	Phe	Thr	Phe
				50					55					60
Pro	Leu	Glu	Thr	Cys	Asn	Ala	Arg	His	Gly	Gly	Ser	Arg	Leu	
				65					70					

<210> 190

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 190

agggaccatt gcttcttcca ggcc 24

<210> 191

<211> 24

<212> DNA

<213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 191
 cgttacatgt ctccaagggg aatg 24

<210> 192
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 192
 cctgtgctaa gtgccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193
 <211> 1091
 <212> DNA
 <213> Homo sapiens

<400> 193
 caagcaggtc atcccccttg tgaccttcaa agagaagcag agagggcaga 50
 ggtggggggc acagggaaag ggtgacctct gagattcccc ttttccccca 100
 gactttggaa gtgaaccacc atggggctca gcatcttttt gctcctgtgt 150
 gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
 gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250
 gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
 gctcactgca gcggcagcag gtactgggtg cgctggggg aacacagcct 350
 cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
 cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450
 ctgctgcggc tgogcctgcc cgtccgcgta accagcagcg ttcaaccct 500
 gcccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550
 gctggggcat caccaaccac ccacggaacc cattcccga tctgctccag 600
 tgcctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650
 cgggagaatc acgagcaaca tgggtgtgtc agggggcgtc ccggggcagg 700
 atgcctgcca gggtgattct gggggccccc tgggtgtgtg gggagtctt 750
 caaggtctgg tgtcctgggg gtctgtgggg cctgtggac aagatggcat 800

ccctggagtc tacacctata ttgcaagta tgtggactgg atccggatga 850
 tcatgaggaa caactgacct gtttcctcca cctccacccc cacccttaa 900
 cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950
 ccctagctcc actcttgttg gcctgggaac ttcttgggaac ttttaactcct 1000
 gccagccctt ctaagaccca cgagcgggggt gagagaagtg tgcaatagtc 1050
 tggaataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194

<211> 248

<212> PRT

<213> Homo sapiens

<400> 194

Met	Gly	Leu	Ser	Ile	Phe	Leu	Leu	Leu	Cys	Val	Leu	Gly	Leu	Ser	1	5	10	15
Gln	Ala	Ala	Thr	Pro	Lys	Ile	Phe	Asn	Gly	Thr	Glu	Cys	Gly	Arg	20	25	30	
Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu	35	40	45	
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala	50	55	60	
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His	65	70	75	
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly	80	85	90	
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His	95	100	105	
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val	110	115	120	
Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	125	130	135	
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	140	145	150	
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	155	160	165	
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	170	175	180	
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	185	190	195	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu				

200	205	210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp		
215	220	225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp		
230	235	240
Ile Arg Met Ile Met Arg Asn Asn		
245		

<210> 195
 <211> 1485
 <212> DNA
 <213> Homo sapiens

<400> 195
 gcggccacac gcagctagcc ggagcccgga ccaggcgcct gtgcctcctc 50
 ctcgctccctc gccgcgtccg cgaagcctgg agccggcggg agccccgcgc 100
 tcgccatgtc gggcgagctc agcaacaggt toccaaggagg gaaggcgttc 150
 ggcttgetca aagcccggca ggagaggagg ctggccgaga tcaaccggga 200
 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350
 caagaccac ctggagatga agaagatgat ctgagagggtg acaggagggg 400
 tcagtgcacac tatatcctac cgagactttg tgaacatgat gctggggaaa 450
 cggtcggctg tcttcaagtt agtcatgatg tttgaaggaa aagccaacga 500
 gagcagcccc aagccagttg gccccctcc agagagagac attgctagcc 550
 tgccctgagg accccgcctg gactcccag ccttcccacc ccatacctcc 600
 ctcccgatct tgctgccctt cttgacacac tgtgatctct ctctctctca 650
 tttgtttggt cattgagggg ttgtttgtgt tttcatcaat gtctttgtaa 700
 agcacaaaatt atctgcctta aaggggctct gggtcgggga atcctgagcc 750
 ttgggtcccc tccctctctt cttccctcct tccccgctcc ctgtgcagaa 800
 gggctgatat caaaccaaaa actagagggg gcagggccag ggcagggagg 850
 cttccagcct gtgttccct cacttgaggg aaccagcact ctccatcctt 900
 tcagaaagtc tocaagccaa gttcaggctc actgacctgg ctctgacgag 950
 gacccaggc cactctgaga agaccttga gtagggacaa ggctgcaggg 1000
 cctctttcgg gtttccttgg acagtgccat gggtccagtg ctctggtgtc 1050

acccaggaca cagccactcg gggccccgct gccccagctg atccccactc 1100
 attccacacc tcttctcatc ctcaagtatg tgaaggtggg aaggaaagga 1150
 gcttggcatt gggagccctt caagaaggta ccagaaggaa ccctccagtc 1200
 ctgctctctg gccacacctg tgcaggcagc tgagaggcag cgtgcagccc 1250
 tactgtccct tactggggca gcagagggct tcggaggcag aagtgaggcc 1300
 tggggtttgg ggggaaaggt cagctcagtg ctgttccacc ttttagggag 1350
 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400
 aagtcagcag cactggtaag ccaagactga gaaatacaag gttgcttgtc 1450
 tgacccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

Met	Ser	Gly	Glu	Leu	Ser	Asn	Arg	Phe	Gln	Gly	Gly	Lys	Ala	Phe
1				5					10					15

Gly	Leu	Leu	Lys	Ala	Arg	Gln	Glu	Arg	Arg	Leu	Ala	Glu	Ile	Asn
				20					25					30

Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu
				35					40					45

Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp
				50					55					60

Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met
				65					70					75

Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys
				80					85					90

Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr
				95					100					105

Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu
				110					115					120

Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro
				125					130					135

Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro
				140					145					150

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

<400> 197

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cagcctctct caggagcggg gccctgcaca ccatggcccc cgggtgggca 100
ggggtcggcg ccgcctgctg cgcgcgcctg gcgctggcct tggcgtggtc 150
gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200
gctccgctgc cagcgtggac tgccacgggc tgggcctccg cgcggttcct 250
cggggcatcc cccgcaacgc tgagcgcctt gacctggaca gaaataatat 300
caccaggatc accaagatgg acttcgctgg gctcaagaac ctccgagtct 350
tgcatctgga agacaaccag gtcagcgtca tcgagagagg cgccttcag 400
gacctgaagc agctagagcg actgcgctg aacaagaata agctgcaagt 450
ccttcagaaa ttgcttttcc agagcacgcc gaagctcacc agactagatt 500
tgagtgaaaa ccagatccag gggatcccga ggaaggcgtt ccgcggcatc 550
accgatgtga agaacctgca actggacaac aaccacatca gctgcattga 600
agatggagcc ttccgagcgc tgcgcgattt ggagatcctt accctcaaca 650
acaacaacat cagtgcctc ctgggtacca gcttcaacca catgccgaag 700
atccgaactc tgcgcctcca ctccaaccac ctctactgcg actgccacct 750
ggcctggctc tcggattggc tgcgacagcg acggacagtt ggccagttca 800
cactctgcat ggctcctgtg catttgaggg gcttcaacgt ggcggatgtg 850
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tcgtggactg tcgaggaaag ggcttgatgg agattcctgc caacttgccg 1000
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 1050
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agaatcagat atcggatatt gctccagatg ccttcaggg cctgaaatca 1150
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ttgctctccc tgtatgacaa caagctgcag accatcagca aggggtcttt 1350
cgcccctctg cagtccatcc agacaactca cttagcccaa aaccatttg 1400
tgtgcgactg ccacttgaag tggctggccg actacctcca ggacaacccc 1450

atcgagacaa gcggggcccc ctgcagcagc ccgcgccgac tcgccaacaa 1500
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 cacctttgcc ggctgagtt cggtagact gctgtccctc tatgacaatc 2000
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 gctcggcaag tggttgagga agaggcggat cgtcagtggg aacctaggt 2150
 gccagaagcc atttttcctc aaggagattc ccatccagga tgtggccatc 2200
 caggacttca cctgtgatgg caacgaggag agtagctgcc agctgagccc 2250
 gcgctgcccc gagcagtga cctgtatgga gacagtgggt cgatgcagca 2300
 acaaggggct ccgcgccctc ccagaggca tgcccaagga tgtgaccgag 2350
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 gttgggacag ccatgtggga cccctggtg attcagcatg aaggaaatga 4750
 agctggagag gaaggtaaag aagaagagaa tattaagtat attgtaaaat 4800
 aaacaaaaaa tagaacttaa aaaaaaaaaa aaaaaaaaaa aa 4842

<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

Met	Ala	Pro	Gly	Trp	Ala	Gly	Val	Gly	Ala	Ala	Val	Arg	Ala	Arg	1	5	10	15
Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Ser	Val	Leu	Ser	Gly	Pro	Pro	20	25	30	
Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val	35	40	45	
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro	50	55	60	
Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg	65	70	75	
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu	80	85	90	
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe	95	100	105	
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys	110	115	120	
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu	125	130	135	
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg	140	145	150	
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp	155	160	165	

Asn	Asn	His	Ile	Ser	Cys	Ile	Glu	Asp	Gly	Ala	Phe	Arg	Ala	Leu	170	175	180
Arg	Asp	Leu	Glu	Ile	Leu	Thr	Leu	Asn	Asn	Asn	Asn	Ile	Ser	Arg	185	190	195
Ile	Leu	Val	Thr	Ser	Phe	Asn	His	Met	Pro	Lys	Ile	Arg	Thr	Leu	200	205	210
Arg	Leu	His	Ser	Asn	His	Leu	Tyr	Cys	Asp	Cys	His	Leu	Ala	Trp	215	220	225
Leu	Ser	Asp	Trp	Leu	Arg	Gln	Arg	Arg	Thr	Val	Gly	Gln	Phe	Thr	230	235	240
Leu	Cys	Met	Ala	Pro	Val	His	Leu	Arg	Gly	Phe	Asn	Val	Ala	Asp	245	250	255
Val	Gln	Lys	Lys	Glu	Tyr	Val	Cys	Pro	Ala	Pro	His	Ser	Glu	Pro	260	265	270
Pro	Ser	Cys	Asn	Ala	Asn	Ser	Ile	Ser	Cys	Pro	Ser	Pro	Cys	Thr	275	280	285
Cys	Ser	Asn	Asn	Ile	Val	Asp	Cys	Arg	Gly	Lys	Gly	Leu	Met	Glu	290	295	300
Ile	Pro	Ala	Asn	Leu	Pro	Glu	Gly	Ile	Val	Glu	Ile	Arg	Leu	Glu	305	310	315
Gln	Asn	Ser	Ile	Lys	Ala	Ile	Pro	Ala	Gly	Ala	Phe	Thr	Gln	Tyr	320	325	330
Lys	Lys	Leu	Lys	Arg	Ile	Asp	Ile	Ser	Lys	Asn	Gln	Ile	Ser	Asp	335	340	345
Ile	Ala	Pro	Asp	Ala	Phe	Gln	Gly	Leu	Lys	Ser	Leu	Thr	Ser	Leu	350	355	360
Val	Leu	Tyr	Gly	Asn	Lys	Ile	Thr	Glu	Ile	Ala	Lys	Gly	Leu	Phe	365	370	375
Asp	Gly	Leu	Val	Ser	Leu	Gln	Leu	Leu	Leu	Leu	Asn	Ala	Asn	Lys	380	385	390
Ile	Asn	Cys	Leu	Arg	Val	Asn	Thr	Phe	Gln	Asp	Leu	Gln	Asn	Leu	395	400	405
Asn	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Lys	Leu	Gln	Thr	Ile	Ser	Lys	410	415	420
Gly	Leu	Phe	Ala	Pro	Leu	Gln	Ser	Ile	Gln	Thr	Leu	His	Leu	Ala	425	430	435
Gln	Asn	Pro	Phe	Val	Cys	Asp	Cys	His	Leu	Lys	Trp	Leu	Ala	Asp	440	445	450
Tyr	Leu	Gln	Asp	Asn	Pro	Ile	Glu	Thr	Ser	Gly	Ala	Arg	Cys	Ser			

455					460					465				
Ser	Pro	Arg	Arg	Leu	Ala	Asn	Lys	Arg	Ile	Ser	Gln	Ile	Lys	Ser
				470					475					480
Lys	Lys	Phe	Arg	Cys	Ser	Gly	Ser	Glu	Asp	Tyr	Arg	Ser	Arg	Phe
				485					490					495
Ser	Ser	Glu	Cys	Phe	Met	Asp	Leu	Val	Cys	Pro	Glu	Lys	Cys	Arg
				500					505					510
Cys	Glu	Gly	Thr	Ile	Val	Asp	Cys	Ser	Asn	Gln	Lys	Leu	Val	Arg
				515					520					525
Ile	Pro	Ser	His	Leu	Pro	Glu	Tyr	Val	Thr	Asp	Leu	Arg	Leu	Asn
				530					535					540
Asp	Asn	Glu	Val	Ser	Val	Leu	Glu	Ala	Thr	Gly	Ile	Phe	Lys	Lys
				545					550					555
Leu	Pro	Asn	Leu	Arg	Lys	Ile	Asn	Leu	Ser	Asn	Asn	Lys	Ile	Lys
				560					565					570
Glu	Val	Arg	Glu	Gly	Ala	Phe	Asp	Gly	Ala	Ala	Ser	Val	Gln	Glu
				575					580					585
Leu	Met	Leu	Thr	Gly	Asn	Gln	Leu	Glu	Thr	Val	His	Gly	Arg	Val
				590					595					600
Phe	Arg	Gly	Leu	Ser	Gly	Leu	Lys	Thr	Leu	Met	Leu	Arg	Ser	Asn
				605					610					615
Leu	Ile	Ser	Cys	Val	Ser	Asn	Asp	Thr	Phe	Ala	Gly	Leu	Ser	Ser
				620					625					630
Val	Arg	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Arg	Ile	Thr	Thr	Ile	Thr
				635					640					645
Pro	Gly	Ala	Phe	Thr	Thr	Leu	Val	Ser	Leu	Ser	Thr	Ile	Asn	Leu
				650					655					660
Leu	Ser	Asn	Pro	Phe	Asn	Cys	Asn	Cys	His	Leu	Ala	Trp	Leu	Gly
				665					670					675
Lys	Trp	Leu	Arg	Lys	Arg	Arg	Ile	Val	Ser	Gly	Asn	Pro	Arg	Cys
				680					685					690
Gln	Lys	Pro	Phe	Phe	Leu	Lys	Glu	Ile	Pro	Ile	Gln	Asp	Val	Ala
				695					700					705
Ile	Gln	Asp	Phe	Thr	Cys	Asp	Gly	Asn	Glu	Glu	Ser	Ser	Cys	Gln
				710					715					720
Leu	Ser	Pro	Arg	Cys	Pro	Glu	Gln	Cys	Thr	Cys	Met	Glu	Thr	Val
				725					730					735
Val	Arg	Cys	Ser	Asn	Lys	Gly	Leu	Arg	Ala	Leu	Pro	Arg	Gly	Met
				740					745					750

Pro Lys Asp Val Thr Glu Leu Tyr Leu Glu Gly Asn His Leu Thr	755	760	765
Ala Val Pro Arg Glu Leu Ser Ala Leu Arg His Leu Thr Leu Ile	770	775	780
Asp Leu Ser Asn Asn Ser Ile Ser Met Leu Thr Asn Tyr Thr Phe	785	790	795
Ser Asn Met Ser His Leu Ser Thr Leu Ile Leu Ser Tyr Asn Arg	800	805	810
Leu Arg Cys Ile Pro Val His Ala Phe Asn Gly Leu Arg Ser Leu	815	820	825
Arg Val Leu Thr Leu His Gly Asn Asp Ile Ser Ser Val Pro Glu	830	835	840
Gly Ser Phe Asn Asp Leu Thr Ser Leu Ser His Leu Ala Leu Gly	845	850	855
Thr Asn Pro Leu His Cys Asp Cys Ser Leu Arg Trp Leu Ser Glu	860	865	870
Trp Val Lys Ala Gly Tyr Lys Glu Pro Gly Ile Ala Arg Cys Ser	875	880	885
Ser Pro Glu Pro Met Ala Asp Arg Leu Leu Leu Thr Thr Pro Thr	890	895	900
His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn Ile Val Ala	905	910	915
Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn Gly Thr	920	925	930
Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro Tyr	935	940	945
Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile	950	955	960
Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser	965	970	975
His Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly	980	985	990
Gln Arg Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys	995	1000	1005
Glu Asn Asn Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys	1010	1015	1020
Ile Cys Pro Pro Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile	1025	1030	1035
Asp His Cys Val Pro Glu Leu Asn Leu Cys Gln His Glu Ala Lys			

1040	1045	1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly		
1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala		
1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly		
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu		
1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln		
1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu		
1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu		
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu		
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln		
1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser	1340	1345	1350
Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp	1355	1360	1365
Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly	1370	1375	1380
Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu	1385	1390	1395
Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn	1400	1405	1410
Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser	1415	1420	1425
Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly	1430	1435	1440
Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg	1445	1450	1455
Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala	1460	1465	1470
Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln	1475	1480	1485
Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln	1490	1495	1500
Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu	1505	1510	1515
Glu Cys Gly Cys Leu Ala Cys Ser	1520		

<210> 199

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 199

atggagattc ctgccaaactt gccg 24

<210> 200

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 200
ttgttggcat tgaggaggag cagc 24

<210> 201
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 201
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202
<211> 753
<212> DNA
<213> Homo sapiens

<400> 202
ggatgcagga cgctcccctg agctgcctgt caccgactag gtggagcagt 50
gtttcttcctg cagactcaac tgagaagtca gcctctgggg caggcaccag 100
gaatctgcct tttcagttct gtctccggca ggctttgagg atgaaggctg 150
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250
caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300
agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350
gactatggca tottocagat caacagcttc gcgtggtgca gacgcggaaa 400
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450
atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500
caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550
cctgtccgag tggaaaaaag gctgtgaggt ttcttaaact ggaactggac 600
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gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaaatt 750
gtc 753

<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 203

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Gly	Ala	Glu	Ser	Lys	Ile	Tyr	Thr	Arg	Cys	Lys	Leu	Ala	Lys	Ile
				20					25					30
Phe	Ser	Arg	Ala	Gly	Leu	Asp	Asn	Tyr	Trp	Gly	Phe	Ser	Leu	Gly
				35					40					45
Asn	Trp	Ile	Cys	Met	Ala	Tyr	Tyr	Glu	Ser	Gly	Tyr	Asn	Thr	Thr
				50					55					60
Ala	Pro	Thr	Val	Leu	Asp	Asp	Gly	Ser	Ile	Asp	Tyr	Gly	Ile	Phe
				65					70					75
Gln	Ile	Asn	Ser	Phe	Ala	Trp	Cys	Arg	Arg	Gly	Lys	Leu	Lys	Glu
				80					85					90
Asn	Asn	His	Cys	His	Val	Ala	Cys	Ser	Ala	Leu	Ile	Thr	Asp	Asp
				95					100					105
Leu	Thr	Asp	Ala	Ile	Ile	Cys	Ala	Arg	Lys	Ile	Val	Lys	Glu	Thr
				110					115					120
Gln	Gly	Met	Asn	Tyr	Trp	Gln	Gly	Trp	Lys	Lys	His	Cys	Glu	Gly
				125					130					135
Arg	Asp	Leu	Ser	Glu	Trp	Lys	Lys	Gly	Cys	Glu	Val	Ser		
				140					145					

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 204

gcaggctttg aggatgaagg ctgc 24

<210> 205

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 205
ctcattggct gcctggtcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 207
tcagtgacca aggctgagca ggcg 24

<210> 208
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 208
ctacactcgt tgcaaactgg caaaaatatt ctcgagggt ggcctgg 47

<210> 209
<211> 1648
<212> DNA
<213> Homo sapiens

<400> 209
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cctcagcagt gtcattgtgt aaaaacgcc aagctgaatat atcatgcccc 100
tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150
ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
gcggaagaag atcctatatt actgtcactt cccagatctg cttctcacca 250

agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300
 gaggaatata ccacaggcat ggcagactgc atcttagtca acagccagtt 350
 cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400
 ctgatgtcct ctatccatct ctaaattgtca ccagctttga ctcatgtgtt 450
 cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgctgct 500
 ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcactggaag 550
 ccctagtaca gctgcgtgga agattgacat cccaagattg ggagagggtt 600
 catctgatcg tggcagggtg ttatgacgag agagtcttg agaattgtga 650
 acattatcag gaattgaaga aaatgggtcca acagtccgac cttggccagt 700
 atgtgacctt cttgaggtct ttctcagaca aacagaaaaat ctccctcctc 750
 cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800
 tgccctctg gaagccatgt acatgcagtg cccagtcatt gctgttaatt 850
 cgggtggacc cttggagtcc attgaccaca gtgtcacagg gtttctgtgt 900
 gagcctgacc cgggtgcactt ctcagaagca atagaaaagt tcatccgtga 950
 accttcctta aaagccacca tgggcctggc tggaagagcc agagtgaagg 1000
 aaaaattttc cctgaagca tttacagaac agctctaccg atatgttacc 1050
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 ttatggattg tagaccaggt tttgaaacca aaaaagaaac ctagaatcta 1150
 atgcagaaga gatcttttaa aaaataaact tgagtcttga atgtgagcca 1200
 ctttctata taccacacct ccctgtccac ttttcagaaa aaccatgtct 1250
 tttatgctat aatcattcca aattttgcca gtgttaagtt acaaattgtg 1300
 tgtcattcca tgttcagcag agtattttta ttatatattt togggattat 1350
 tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggttttc 1400
 atagtttaag tgtgtatcat tatcaaagtt gattaatttg gcttcatagt 1450
 ataattgagag cagggtctatt gtagttccca gattcaatcc accgaagtgt 1500
 tcaactgtcat ctgttaggga atttttgttt gtccgtgtct tgcctggatc 1550
 catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600
 actgagatat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaaaa 1648

<210> 210

<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly
1 5 10 15
Glu Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val
20 25 30
Phe Arg Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His
35 40 45
Phe Pro Asp Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg
50 55 60
Leu Tyr Arg Ala Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly
65 70 75
Met Ala Asp Cys Ile Leu Val Asn Ser Gln Phe Thr Ala Ala Val
80 85 90
Phe Lys Glu Thr Phe Lys Ser Leu Ser His Ile Asp Pro Asp Val
95 100 105
Leu Tyr Pro Ser Leu Asn Val Thr Ser Phe Asp Ser Val Val Pro
110 115 120
Glu Lys Leu Asp Asp Leu Val Pro Lys Gly Lys Lys Phe Leu Leu
125 130 135
Leu Ser Ile Asn Arg Tyr Glu Arg Lys Lys Asn Leu Thr Leu Ala
140 145 150
Leu Glu Ala Leu Val Gln Leu Arg Gly Arg Leu Thr Ser Gln Asp
155 160 165
Trp Glu Arg Val His Leu Ile Val Ala Gly Gly Tyr Asp Glu Arg
170 175 180
Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys Lys Met Val
185 190 195
Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg Ser Phe
200 205 210
Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys Val
215 220 225
Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu
230 235 240
Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly
245 250 255
Pro Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu
260 265 270

Pro	Asp	Pro	Val	His	Phe	Ser	Glu	Ala	Ile	Glu	Lys	Phe	Ile	Arg
				275					280					285
Glu	Pro	Ser	Leu	Lys	Ala	Thr	Met	Gly	Leu	Ala	Gly	Arg	Ala	Arg
				290					295					300
Val	Lys	Glu	Lys	Phe	Ser	Pro	Glu	Ala	Phe	Thr	Glu	Gln	Leu	Tyr
				305					310					315
Arg	Tyr	Val	Thr	Lys	Leu	Leu	Val							
				320										

<210> 211
 <211> 1554
 <212> DNA
 <213> Homo sapiens

<400> 211
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 tctacoteta tccggcttcc agacaagctg caggaattcc agggattact 150
 ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtgaag 200
 tttgcatgag ttcctgggta atttgcata gagatatggg cctgtggtct 250
 ccttctggtt tggcaggcgc ctcgtgggta gtttgggcac tgttgatgta 300
 ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350
 gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaag 400
 accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
 agtaactttg cctcctcct aaagctttca gaagaattat tagataaatg 500
 gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550
 gttttgctat gaagtctggt acacagatgg taatgggtag tacatttgaa 600
 gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650
 tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700
 ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750
 aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800
 tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850
 gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
 tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950
 tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050
 gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100
 tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150
 tggtagttca ggatcctaact acttgcccat ctccacacaa gtttgatcca 1200
 gatcggtttg atgatgaatt agtaatgaaa actttttcct cacttggatt 1250
 ctcaggcaca caggagtgtc cagagttgag gtttgcatat atggtgacca 1300
 cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350
 ggacagggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400
 agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450
 cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550
 ttaa 1554

<210> 212
 <211> 462
 <212> PRT
 <213> Homo sapiens

<400> 212
 Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu
 1 5 10 15
 Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala
 20 25 30
 Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu
 35 40 45
 Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn
 50 55 60
 Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg
 65 70 75
 Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His
 80 85 90
 Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys
 95 100 105
 Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn
 110 115 120
 His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu
 125 130 135
 Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu

140	145	150
Asp Lys Trp Leu Ser Tyr Pro Glu Thr	Gln His Val Pro Leu Ser	
155	160	165
Gln His Met Leu Gly Phe Ala Met Lys	Ser Val Thr Gln Met Val	
170	175	180
Met Gly Ser Thr Phe Glu Asp Asp Gln	Glu Val Ile Arg Phe Gln	
185	190	195
Lys Asn His Gly Thr Val Trp Ser Glu	Ile Gly Lys Gly Phe Leu	
200	205	210
Asp Gly Ser Leu Asp Lys Asn Met Thr	Arg Lys Lys Gln Tyr Glu	
215	220	225
Asp Ala Leu Met Gln Leu Glu Ser Val	Leu Arg Asn Ile Ile Lys	
230	235	240
Glu Arg Lys Gly Arg Asn Phe Ser Gln	His Ile Phe Ile Asp Ser	
245	250	255
Leu Val Gln Gly Asn Leu Asn Asp Gln	Gln Ile Leu Glu Asp Ser	
260	265	270
Met Ile Phe Ser Leu Ala Ser Cys Ile	Ile Thr Ala Lys Leu Cys	
275	280	285
Thr Trp Ala Ile Cys Phe Leu Thr Thr	Ser Glu Glu Val Gln Lys	
290	295	300
Lys Leu Tyr Glu Glu Ile Asn Gln Val	Phe Gly Asn Gly Pro Val	
305	310	315
Thr Pro Glu Lys Ile Glu Gln Leu Arg	Tyr Cys Gln His Val Leu	
320	325	330
Cys Glu Thr Val Arg Thr Ala Lys Leu	Thr Pro Val Ser Ala Gln	
335	340	345
Leu Gln Asp Ile Glu Gly Lys Ile Asp	Arg Phe Ile Ile Pro Arg	
350	355	360
Glu Thr Leu Val Leu Tyr Ala Leu Gly	Val Val Leu Gln Asp Pro	
365	370	375
Asn Thr Trp Pro Ser Pro His Lys Phe	Asp Pro Asp Arg Phe Asp	
380	385	390
Asp Glu Leu Val Met Lys Thr Phe Ser	Ser Leu Gly Phe Ser Gly	
395	400	405
Thr Gln Glu Cys Pro Glu Leu Arg Phe	Ala Tyr Met Val Thr Thr	
410	415	420
Val Leu Leu Ser Val Leu Val Lys Arg	Leu His Leu Leu Ser Val	
425	430	435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
455 460

<210> 213

<211> 759

<212> DNA

<213> Homo sapiens

<400> 213

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tccagcctca gagaccgccg cccttgtccc cgagggccat gggccgggtc 100
tcagggttg tgccctctcg ctctctgacg ctctgggcgc atctggtggt 150
cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200
ctctcacgtt caccocogag gagtatgaca agcaggacat tcagctggtg 250
gccgcgtct ctgtcaccct gggcctcttt gcagtggagc tggccgggtt 300
cctctcagga gtctocatgt tcaacagcac ccagagcctc atctccattg 350
gggctcactg tagtgcattc gtggccctgt ccttcttcat attcgagcgt 400
tgaggagtga ctacgtattg gtacatcttt gtcttctgca gtgcccttcc 450
agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500
aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550
ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600
ttccctcgg aaactgcttc tgctggagga tatgtgttg aataattacg 650
tcttgagtct gggattatcc gcattgtatt tagtgcttg taataaaata 700
tgttttgtag taacattaag acttatatac agttttaggg gacaattaa 750
aaaaaaaa 759

<210> 214

<211> 140

<212> PRT

<213> Homo sapiens

<400> 214

Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
1 5 10 15
Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
20 25 30
Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
35 40 45

Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
 50 55 60
 Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
 65 70 75
 Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
 80 85 90
 Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
 95 100 105
 Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
 110 115 120
 Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
 125 130 135
 Lys Lys Lys Pro Phe
 140

<210> 215
 <211> 697
 <212> DNA
 <213> Homo sapiens

<400> 215
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 cctgggctct cccagacctc ctctgactcg gagcggctca ggagacagaa 100
 gacccggcct gctgcagccc catagtgtccc cggaacgagt ggaaggccct 150
 ggcacacagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200
 tatcgcacac ggcgggcagc agctgcaaca ccccgacctc gtgccagcag 250
 caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300
 cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
 gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
 tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450
 ccaggccatc cgggcagccc aggtctact ggctgcgggt gtggctcagg 500
 gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550
 aactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600
 ctaccgctcc cctgagggcc ctgctgatcc gcacccatt cctcccctcc 650
 catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216
 <211> 196
 <212> PRT

<213> Homo sapiens

<400> 216

Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu
1 5 10 15
Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys
20 25 30
Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu
35 40 45
Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser
50 55 60
His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln
65 70 75
Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp
80 85 90
Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val
95 100 105
Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His
110 115 120
Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr
125 130 135
Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly
140 145 150
Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr
155 160 165
Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly
170 175 180
Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser
185 190 195
Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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tctatctggt catctgtggc caggatgatg gtcctcccgg ctgagaggac 150
cctgagcgtg atgaccacga gggccagccc cggccccggg tgcctcgga 200

gcggggccac atctcaccta agtcccgcgc catggccaat tccactctcc 250
 tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc 300
 cccaaccgcc cgaaccacag cccccacccc tcagccaagg tgaagaaaat 350
 ctttggctgg ggcgacttct actccaacat caagacggtg gccctgaacc 400
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 aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600
 gaacgggggc gccggacctc gctttgcacc cagcaccag ccaagatctg 650
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 tcaaagtcgt ctgtgtctac atgccttct acagcacgga ctatcggtg 750
 gtccagaagg tgtgccaga ttacaactac catagtata cccctacta 800
 cccatctggg tgaccggggg caggccacag agggcaggcc agggctggaa 850
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 gttgggcctc aggcaggag gggggtggag acgaggagat gccaagtggg 950
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 aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagt 1050
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tcacctgtca gaccgggggtt ctcccggtac tggatggcgc cgccctctca 1700
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 aataaagctt gccccggggc a 1871

<210> 218
 <211> 252
 <212> PRT
 <213> Homo sapiens

<400> 218

Met	Gln	Leu	Thr	Arg	Cys	Cys	Phe	Val	Phe	Leu	Val	Gln	Gly	Ser	1	5	10	15
Leu	Tyr	Leu	Val	Ile	Cys	Gly	Gln	Asp	Asp	Gly	Pro	Pro	Gly	Ser	20	25	30	
Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg	35	40	45	
Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met	50	55	60	
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala	65	70	75	
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro	80	85	90	
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe	95	100	105	
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly	110	115	120	
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln	125	130	135	
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro	140	145	150	
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile	155	160	165	
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu	170	175	180	
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro	185	190	195	
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp	200	205	210	

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
 215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
 230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
 245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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 gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150
 agctcgaggg gagactttga cttcaagcca cagaattggg ggaagtgtgc 200
 gcgcgcgcgc cgccgtcgtc cctgcagcgc tgtcgacctt gccgctagca 250
 tcttcccgag caccgggatc ccggggtagg aggcgacgcg ggcgagcacc 300
 agcgcagacc ggctgcggct gccacacagg ctcaccatgg gctccgggcg 350
 ccgggcgctg tccgcggtgc cggccgtgct gctggctctc acgctgcccg 400
 ggctgcccgct ctgggcacag aacgacacgg agcccatcgt gctggagggc 450
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 ctcttctctc ccgctgggga tatcggtccg ggccggccaac tccaaggtcg 550
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 aagacgcgca tcatttactt cgatcagatc ctggtgaatg tgggtaattt 650
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 ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaaga 800
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 aagcagataa tacctatgct taaatgtaac agtcaaaaagc tgtctgcaag 1200
 acttattctg aatttcattt cctgggatta ctgaattagt tacagatgtg 1250
 gaattttatt tgttttagttt taaaagactg gcaaccaggt ctaaggatta 1300
 gaaaactcta aagttctgac ttcaatcaac ggtagtggtg atactgccaa 1350
 agaactgtat actgtgttaa tatattgatt atatttgttt ttattccttt 1400
 ggaattagtt tgtttggttc ttgtaaaaaa cttggatttt ttttttcagt 1450
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 gaatgcttca tagttgtatt ttaattgtat atgtgaaaga gtcattttt 1600
 ccaagttata ttttctaaga agaagaatag atcataaatc tgacaaggaa 1650
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 cagctcccct ccgagggaaa tottatactt tattgctcaa ctttaattaa 1750
 aatgattgat aataaccact ttattaaaaa cctaagggtt ttttttttc 1800
 cgtagacatg accactttat taactggtgg tgggatgctg ttgtttctaa 1850
 ttatacctat ttttcaaggc ttctgttgta tttgaagtat catctggtt 1900
 tgccttaact ctttaaattg tatatattta tctgttttagc taatattaa 1950
 ttcaaataac ccatatctaa atttagtgca atatcttgct tttgtatag 2000
 gtcatatgaa ttcataaaat tatttatgtc tgttatagaa taaagattaa 2050
 tatatgttaa aaaaa 2065

<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

Met	Gly	Ser	Gly	Arg	Arg	Ala	Leu	Ser	Ala	Val	Pro	Ala	Val	Leu
1				5				10						15

Leu	Val	Leu	Thr	Leu	Pro	Gly	Leu	Pro	Val	Trp	Ala	Gln	Asn	Asp
			20					25						30

Thr	Glu	Pro	Ile	Val	Leu	Glu	Gly	Lys	Cys	Leu	Val	Val	Cys	Asp
			35					40						45

Ser	Asn	Pro	Ala	Thr	Asp	Ser	Lys	Gly	Ser	Ser	Ser	Ser	Pro	Leu
			50					55						60

Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	
				65					70					75	
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	
				80					85					90	
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	
				95					100					105	
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	
				110					115					120	
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	
				125					130					135	
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	
				140					145					150	
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	
				155					160					165	
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu	
				170					175					180	
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly	
				185					190					195	
Phe	Leu	Val	Phe	Pro	Leu										
				200											

<210> 221

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 221

acggctcacc atgggctccg 20

<210> 222

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 222

aggaagagga gccottggag tccg 24

<210> 223

<211> 40

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 223
cggtgctggag ggcaagtgtc tgggtggtgtg cgactcgaac 40

<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

<400> 224
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tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200
ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250
tatccaagaa atgttccgat ttgcatatta taaactctta aaaaaagcca 300
gtgaagggtt gaagagtata aaccaggtg agacagcacc ctctatgca 350
ctgctggcct atgtttctgg ctgggcttt ggaatcatga gtggagtatt 400
ttcctttgtg aataccctat ctgactcctt ggggccaggc acagtgggca 450
ttcatggaga ttctcctcaa ttcttccttt attcagcttt catgacgctg 500
gtcattatct tgctgcatgt attctggggc attgtatttt ttgatggctg 550
tgagaagaaa aagtggggca tcctccttat cgttctcctg acccacctgc 600
tgggtgtcagc ccagaccttc ataagttctt attatggaat aaacctggcg 650
tcagcattta taatcctggt gctcatgggc acctgggcat tcttagctgc 700
gggaggcagc tgccgaagcc tgaaactctg cctgctctgc caagacaaga 750
actttcttct ttacaaccag cgctccagat aacctcaggg aaccagcact 800
tcccaaaccg cagactacat ctttagagga agcacaactg tgcctttttc 850
tgaaaatccc tttttctggt ggaattgaga aagaaataaa actatgcaga 900
ta 902

<210> 225
<211> 257
<212> PRT

<213> Homo sapiens

<400> 225

Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly
1 5 10 15
Pro Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Ile Glu Pro Leu
20 25 30
Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser
35 40 45
Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile
50 55 60
Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly
65 70 75
Ala Phe Val Ser Val Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr
80 85 90
Tyr Lys Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn
95 100 105
Pro Gly Glu Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser
110 115 120
Gly Leu Gly Phe Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn
125 130 135
Thr Leu Ser Asp Ser Leu Gly Pro Gly Thr Val Gly Ile His Gly
140 145 150
Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala Phe Met Thr Leu Val
155 160 165
Ile Ile Leu Leu His Val Phe Trp Gly Ile Val Phe Phe Asp Gly
170 175 180
Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val Leu Leu Thr
185 190 195
His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr Tyr Gly
200 205 210
Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly Thr
215 220 225
Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu
230 235 240
Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr Asn Gln Arg
245 250 255
Ser Arg

<210> 226

<211> 3939
<212> DNA
<213> Homo sapiens

<400> 226

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atgttcgctc tgggcttgcc cttcttggtg ctcttggtgg cctcggtcga 100
gagccatctg ggggttctgg ggccaagaa cgtctcgag aaagacgccg 150
agtttgagcg cacctacgtg gacgaggtca acagcgagct ggtcaacatc 200
tacaccttca accatactgt gacccgcaac aggacagagg gcgtgcgtgt 250
gtctgtgaac gtctgaaca agcagaaggg ggcgcggttg ctgtttgtgg 300
tccgccagaa ggaggctgtg gtgtccttcc aggtgccoct aatcctgcga 350
gggatgtttc agcgcaagta cctctaccaa aaagtggaac gaaccctgtg 400
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tgtccaccct gtcaccagtc aacaccacat accagctccg ggtcagccgc 500
atggacgatt ttgtgctcag gactggggag cagttcagct tcaataccac 550
agcagcacag cccagttact tcaagtatga gttccctgaa ggcgtggact 600
cggtaatgt caaggtgacc tccaacaagg ccttccoctg ctcagtcac 650
tccattcagg atgtgctgtg tctgtctat gacctggaca acaacgtagc 700
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cctgccaga aagcggtcac cctcgagtcc tggctgattc ttttctggc 1100
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 tgcattcaat aaacaaccag actcaaaaaa aaaaaaaaaa 3939

<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

Met	Phe	Ala	Leu	Gly	Leu	Pro	Phe	Leu	Val	Leu	Leu	Val	Ala	Ser
1				5					10					15
Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln
				20					25					30

Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser	35	40	45
Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn	50	55	60
Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln	65	70	75
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val	80	85	90
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg	95	100	105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro	110	115	120
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser	125	130	135
Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg	140	145	150
Met	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn	155	160	165
Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu	170	175	180
Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe	185	190	195
Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr	200	205	210
Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	Met	215	220	225
Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser	230	235	240
Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala	245	250	255
Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	Pro	260	265	270
Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	Ser	275	280	285
Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	Phe	Cys	290	295	300
Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu	Ala	305	310	315
Cys	Trp	Glu	Asn	Trp	Arg	Gln	Lys	Lys	Lys	Thr	Leu	Leu	Val	Ala			

320	325	330
Ile Asp Arg Ala Cys Pro Glu Ser Gly	His Pro Arg Val Leu Ala	
335	340	345
Asp Ser Phe Pro Gly Ser Ser Pro Tyr	Glu Gly Tyr Asn Tyr Gly	
350	355	360
Ser Phe Glu Asn Val Ser Gly Ser Thr	Asp Gly Leu Val Asp Ser	
365	370	375
Ala Gly Thr Gly Asp Leu Ser Tyr Gly	Tyr Gln Gly Arg Ser Phe	
380	385	390
Glu Pro Val Gly Thr Arg Pro Arg Val	Asp Ser Met Ser Ser Val	
395	400	405
Glu Glu Asp Asp Tyr Asp Thr Leu Thr	Asp Ile Asp Ser Asp Lys	
410	415	420
Asn Val Ile Arg Thr Lys Gln Tyr Leu	Tyr Val Ala Asp Leu Ala	
425	430	435
Arg Lys Asp Lys Arg Val Leu Arg Lys	Lys Tyr Gln Ile Tyr Phe	
440	445	450
Trp Asn Ile Ala Thr Ile Ala Val Phe	Tyr Ala Leu Pro Val Val	
455	460	465
Gln Leu Val Ile Thr Tyr Gln Thr Val	Val Asn Val Thr Gly Asn	
470	475	480
Gln Asp Ile Cys Tyr Tyr Asn Phe Leu	Cys Ala His Pro Leu Gly	
485	490	495
Asn Leu Ser Ala Phe Asn Asn Ile Leu	Ser Asn Leu Gly Tyr Ile	
500	505	510
Leu Leu Gly Leu Leu Phe Leu Leu Ile	Ile Leu Gln Arg Glu Ile	
515	520	525
Asn His Asn Arg Ala Leu Leu Arg Asn	Asp Leu Cys Ala Leu Glu	
530	535	540
Cys Gly Ile Pro Lys His Phe Gly Leu	Phe Tyr Ala Met Gly Thr	
545	550	555
Ala Leu Met Met Glu Gly Leu Leu Ser	Ala Cys Tyr His Val Cys	
560	565	570
Pro Asn Tyr Thr Asn Phe Gln Phe Asp	Thr Ser Phe Met Tyr Met	
575	580	585
Ile Ala Gly Leu Cys Met Leu Lys Leu	Tyr Gln Lys Arg His Pro	
590	595	600
Asp Ile Asn Ala Ser Ala Tyr Ser Ala	Tyr Ala Cys Leu Ala Ile	
605	610	615

Val	Ile	Phe	Phe	Ser	Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn	
				620					625					630	
Thr	Ala	Phe	Trp	Ile	Val	Phe	Ser	Ile	Ile	His	Ile	Ile	Ala	Thr	
				635					640					645	
Leu	Leu	Leu	Ser	Thr	Gln	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu	
				650					655					660	
Asp	Ser	Gly	Ile	Phe	Arg	Arg	Ile	Leu	His	Val	Leu	Tyr	Thr	Asp	
				665					670					675	
Cys	Ile	Arg	Gln	Cys	Ser	Gly	Pro	Leu	Tyr	Val	Asp	Arg	Met	Val	
				680					685					690	
Leu	Leu	Val	Met	Gly	Asn	Val	Ile	Asn	Trp	Ser	Leu	Ala	Ala	Tyr	
				695					700					705	
Gly	Leu	Ile	Met	Arg	Pro	Asn	Asp	Phe	Ala	Ser	Tyr	Leu	Leu	Ala	
				710					715					720	
Ile	Gly	Ile	Cys	Asn	Leu	Leu	Leu	Tyr	Phe	Ala	Phe	Tyr	Ile	Ile	
				725					730					735	
Met	Lys	Leu	Arg	Ser	Gly	Glu	Arg	Ile	Lys	Leu	Ile	Pro	Leu	Leu	
				740					745					750	
Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe	
				755					760					765	
Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser	
				770					775					780	
Arg	Glu	His	Asn	Arg	Asp	Cys	Ile	Leu	Leu	Asp	Phe	Phe	Asp	Asp	
				785					790					795	
His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser	
				800					805					810	
Phe	Leu	Val	Leu	Leu	Thr	Leu	Asp	Asp	Asp	Leu	Asp	Thr	Val	Gln	
				815					820					825	
Arg	Asp	Lys	Ile	Tyr	Val	Phe									
				830											

<210> 228
 <211> 2848
 <212> DNA
 <213> Homo sapiens

<400> 228
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 ttgggcgctg gagggcctgt cctgaccatg gtccctgcct ggctgtggct 150
 gctttgtgtc tccgtcccc aggctctccc caaggccag cctgcagagc 200

20	25	30
Glu Asn Tyr Gly Gly Asn Phe Pro Leu Tyr Leu Thr Lys Leu Pro 35 40 45		
Leu Pro Arg Glu Gly Ala Glu Gly Gln Ile Val Leu Ser Gly Asp 50 55 60		
Ser Gly Lys Ala Thr Glu Gly Pro Phe Ala Met Asp Pro Asp Ser 65 70 75		
Gly Phe Leu Leu Val Thr Arg Ala Leu Asp Arg Glu Glu Gln Ala 80 85 90		
Glu Tyr Gln Leu Gln Val Thr Leu Glu Met Gln Asp Gly His Val 95 100 105		
Leu Trp Gly Pro Gln Pro Val Leu Val His Val Lys Asp Glu Asn 110 115 120		
Asp Gln Val Pro His Phe Ser Gln Ala Ile Tyr Arg Ala Arg Leu 125 130 135		
Ser Arg Gly Thr Arg Pro Gly Ile Pro Phe Leu Phe Leu Glu Ala 140 145 150		
Ser Asp Arg Asp Glu Pro Gly Thr Ala Asn Ser Asp Leu Arg Phe 155 160 165		
His Ile Leu Ser Gln Ala Pro Ala Gln Pro Ser Pro Asp Met Phe 170 175 180		
Gln Leu Glu Pro Arg Leu Gly Ala Leu Ala Leu Ser Pro Lys Gly 185 190 195		
Ser Thr Ser Leu Asp His Ala Leu Glu Arg Thr Tyr Gln Leu Leu 200 205 210		
Val Gln Val Lys Asp Met Gly Asp Gln Ala Ser Gly His Gln Ala 215 220 225		
Thr Ala Thr Val Glu Val Ser Ile Ile Glu Ser Thr Trp Val Ser 230 235 240		
Leu Glu Pro Ile His Leu Ala Glu Asn Leu Lys Val Leu Tyr Pro 245 250 255		
His His Met Ala Gln Val His Trp Ser Gly Gly Asp Val His Tyr 260 265 270		
His Leu Glu Ser His Pro Pro Gly Pro Phe Glu Val Asn Ala Glu 275 280 285		
Gly Asn Leu Tyr Val Thr Arg Glu Leu Asp Arg Glu Ala Gln Ala 290 295 300		
Glu Tyr Leu Leu Gln Val Arg Ala Gln Asn Ser His Gly Glu Asp 305 310 315		

Tyr Ala Ala Pro	Leu Glu Leu His Val	Leu Val Met Asp Glu Asn	
	320	325	330
Asp Asn Val Pro	Ile Cys Pro Pro Arg	Asp Pro Thr Val Ser Ile	
	335	340	345
Pro Glu Leu Ser	Pro Pro Gly Thr Glu	Val Thr Arg Leu Ser Ala	
	350	355	360
Glu Asp Ala Asp	Ala Pro Gly Ser Pro	Asn Ser His Val Val Tyr	
	365	370	375
Gln Leu Leu Ser	Pro Glu Pro Glu Asp	Gly Val Glu Gly Arg Ala	
	380	385	390
Phe Gln Val Asp	Pro Thr Ser Gly Ser	Val Thr Leu Gly Val Leu	
	395	400	405
Pro Leu Arg Ala	Gly Gln Asn Ile Leu	Leu Leu Val Leu Ala Met	
	410	415	420
Asp Leu Ala Gly	Ala Glu Gly Gly Phe	Ser Ser Thr Cys Glu Val	
	425	430	435
Glu Val Ala Val	Thr Asp Ile Asn Asp	His Ala Pro Glu Phe Ile	
	440	445	450
Thr Ser Gln Ile	Gly Pro Ile Ser Leu	Pro Glu Asp Val Glu Pro	
	455	460	465
Gly Thr Leu Val	Ala Met Leu Thr Ala	Ile Asp Ala Asp Leu Glu	
	470	475	480
Pro Ala Phe Arg	Leu Met Asp Phe Ala	Ile Glu Arg Gly Asp Thr	
	485	490	495
Glu Gly Thr Phe	Gly Leu Asp Trp Glu	Pro Asp Ser Gly His Val	
	500	505	510
Arg Leu Arg Leu	Cys Lys Asn Leu Ser	Tyr Glu Ala Ala Pro Ser	
	515	520	525
His Glu Val Val	Val Val Val Gln Ser	Val Ala Lys Leu Val Gly	
	530	535	540
Pro Gly Pro Gly	Pro Gly Ala Thr Ala	Thr Val Thr Val Leu Val	
	545	550	555
Glu Arg Val Met	Pro Pro Pro Lys Leu	Asp Gln Glu Ser Tyr Glu	
	560	565	570
Ala Ser Val Pro	Ile Ser Ala Pro Ala	Gly Ser Phe Leu Leu Thr	
	575	580	585
Ile Gln Pro Ser	Asp Pro Ile Ser Arg	Thr Leu Arg Phe Ser Leu	
	590	595	600
Val Asn Asp Ser	Glu Gly Trp Leu Cys	Ile Glu Lys Phe Ser Gly	

605	610	615
Glu Val His Thr Ala Gln Ser Leu Gln Gly	Ala Gln Pro Gly Asp	
620	625	630
Thr Tyr Thr Val Leu Val Glu Ala Gln Asp	Thr Ala Leu Thr Leu	
635	640	645
Ala Pro Val Pro Ser Gln Tyr Leu Cys Thr	Pro Arg Gln Asp His	
650	655	660
Gly Leu Ile Val Ser Gly Pro Ser Lys Asp	Pro Asp Leu Ala Ser	
665	670	675
Gly His Gly Pro Tyr Ser Phe Thr Leu Gly	Pro Asn Pro Thr Val	
680	685	690
Gln Arg Asp Trp Arg Leu Gln Thr Leu Asn	Gly Ser His Ala Tyr	
695	700	705
Leu Thr Leu Ala Leu His Trp Val Glu Pro	Arg Glu His Ile Ile	
710	715	720
Pro Val Val Val Ser His Asn Ala Gln Met	Trp Gln Leu Leu Val	
725	730	735
Arg Val Ile Val Cys Arg Cys Asn Val Glu	Gly Gln Cys Met Arg	
740	745	750
Lys Val Gly Arg Met Lys Gly Met Pro Thr	Lys Leu Ser Ala Val	
755	760	765
Gly Ile Leu Val Gly Thr Leu Val Ala Ile	Gly Ile Phe Leu Ile	
770	775	780
Leu Ile Phe Thr His Trp Thr Met Ser Arg	Lys Lys Asp Pro Asp	
785	790	795
Gln Pro Ala Asp Ser Val Pro Leu Lys Ala	Thr Val	
800	805	

<210> 230

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 230

cgcccttaccg cgcagcccgga agattcacta tgggtgaaaat cgccttcaat 50

<210> 231

<211> 24

<212> DNA

<213> Artificial Sequeunce

<220>
 <221> Artificial Sequence
 <222> full
 <223> Synthetic oligonucleotide probe

<400> 231
 cctgagctgt aacccactc cagg 24

<210> 232
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 232
 agagtctgtc ccagctatct tgt 23

<210> 233
 <211> 2786
 <212> DNA
 <213> Homo sapiens

<400> 233
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 acttgaagct caattttctgg aaatctccct cctccttcaa tcggcctgtg 200
 gatgtcctgg tcccatctgt cagtctgcag gcatttaaata ccttcctgag 250
 atcccagggc ttagagtacg cagtgacaat tgaggacctg caggcccttt 300
 tagacaatga agatgatgaa atgcaacaca atgaaggga agaacggagc 350
 agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400
 cgagatggac aacattgccg cagactttcc tgacctggcg aggagggtga 450
 agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500
 actgggaaag gcgtgaggcg gccggccgtt tggtgaatg caggcatcca 550
 ttcccagagag tggatctccc aggccactgc aatctggacg gcaaggaaga 600
 ttgtatctga ttaccagagg gatccagcta tcacctccat cttggagaaa 650
 atggatattt tcttggtgcc tgtggccaat cctgatggat atgtgtatac 700
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 gtcctgcat tgggtgctgac ccaaatagaa actggaacgc tagttttgca 800
 ggaaagggag ccagcgacaa cccttgcctc gaagtgtacc atggaccca 850

cgccaattcg gaagtggagg tgaaatcagt ggtagatttc atccaaaaac 900
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<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

Met	Arg	Trp	Ile	Leu	Phe	Ile	Gly	Ala	Leu	Ile	Gly	Ser	Ser	Ile
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Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn
				20					25					30
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn
				35					40					45
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe
				50					55					60
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala
				65					70					75
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr
				80					85					90
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met
				95					100					105
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr
				110					115					120
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn
				125					130					135
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly
				140					145					150
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr
				155					160					165

Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile	170	175	180
His	Ser	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala	185	190	195
Arg	Lys	Ile	Val	Ser	Asp	Tyr	Gln	Arg	Asp	Pro	Ala	Ile	Thr	Ser	200	205	210
Ile	Leu	Glu	Lys	Met	Asp	Ile	Phe	Leu	Leu	Pro	Val	Ala	Asn	Pro	215	220	225
Asp	Gly	Tyr	Val	Tyr	Thr	Gln	Thr	Gln	Asn	Arg	Leu	Trp	Arg	Lys	230	235	240
Thr	Arg	Ser	Arg	Asn	Pro	Gly	Ser	Ser	Cys	Ile	Gly	Ala	Asp	Pro	245	250	255
Asn	Arg	Asn	Trp	Asn	Ala	Ser	Phe	Ala	Gly	Lys	Gly	Ala	Ser	Asp	260	265	270
Asn	Pro	Cys	Ser	Glu	Val	Tyr	His	Gly	Pro	His	Ala	Asn	Ser	Glu	275	280	285
Val	Glu	Val	Lys	Ser	Val	Val	Asp	Phe	Ile	Gln	Lys	His	Gly	Asn	290	295	300
Phe	Lys	Gly	Phe	Ile	Asp	Leu	His	Ser	Tyr	Ser	Gln	Leu	Leu	Met	305	310	315
Tyr	Pro	Tyr	Gly	Tyr	Ser	Val	Lys	Lys	Ala	Pro	Asp	Ala	Glu	Glu	320	325	330
Leu	Asp	Lys	Val	Ala	Arg	Leu	Ala	Ala	Lys	Ala	Leu	Ala	Ser	Val	335	340	345
Ser	Gly	Thr	Glu	Tyr	Gln	Val	Gly	Pro	Thr	Cys	Thr	Thr	Val	Tyr	350	355	360
Pro	Ala	Ser	Gly	Ser	Ser	Ile	Asp	Trp	Ala	Tyr	Asp	Asn	Gly	Ile	365	370	375
Lys	Phe	Ala	Phe	Thr	Phe	Glu	Leu	Arg	Asp	Thr	Gly	Thr	Tyr	Gly	380	385	390
Phe	Leu	Leu	Pro	Ala	Asn	Gln	Ile	Ile	Pro	Thr	Ala	Glu	Glu	Thr	395	400	405
Trp	Leu	Gly	Leu	Lys	Thr	Ile	Met	Glu	His	Val	Arg	Asp	Asn	Leu	410	415	420

Tyr

<210> 235
 <211> 1743
 <212> DNA
 <213> Homo sapiens

<400> 235

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cccgcccttc ctccacaaag agcaccctg cctcacaggt gtattccctc 200
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 236

Met	Ala	Ser	Tyr	Leu	Tyr	Gly	Val	Leu	Phe	Ala	Val	Gly	Leu	Cys
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Ala	Pro	Ile	Tyr	Cys	Val	Ser	Pro	Ala	Asn	Ala	Pro	Ser	Ala	Tyr
				20					25					30
Pro	Arg	Pro	Ser	Ser	Thr	Lys	Ser	Thr	Pro	Ala	Ser	Gln	Val	Tyr
				35					40					45
Ser	Leu	Asn	Thr	Asp	Phe	Ala	Phe	Arg	Leu	Tyr	Arg	Arg	Leu	Val
				50					55					60
Leu	Glu	Thr	Pro	Ser	Gln	Asn	Ile	Phe	Phe	Ser	Pro	Val	Ser	Val
				65					70					75
Ser	Thr	Ser	Leu	Ala	Met	Leu	Ser	Leu	Gly	Ala	His	Ser	Val	Thr
				80					85					90
Lys	Thr	Gln	Ile	Leu	Gln	Gly	Leu	Gly	Phe	Asn	Leu	Thr	His	Thr
				95					100					105
Pro	Glu	Ser	Ala	Ile	His	Gln	Gly	Phe	Gln	His	Leu	Val	His	Ser
				110					115					120
Leu	Thr	Val	Pro	Ser	Lys	Asp	Leu	Thr	Leu	Lys	Met	Gly	Ser	Ala
				125					130					135
Leu	Phe	Val	Lys	Lys	Glu	Leu	Gln	Leu	Gln	Ala	Asn	Phe	Leu	Gly
				140					145					150
Asn	Val	Lys	Arg	Leu	Tyr	Glu	Ala	Glu	Val	Phe	Ser	Thr	Asp	Phe
				155					160					165
Ser	Asn	Pro	Ser	Ile	Ala	Gln	Ala	Arg	Ile	Asn	Ser	His	Val	Lys
				170					175					180
Lys	Lys	Thr	Gln	Gly	Lys	Val	Val	Asp	Ile	Ile	Gln	Gly	Leu	Asp
				185					190					195
Leu	Leu	Thr	Ala	Met	Val	Leu	Val	Asn	His	Ile	Phe	Phe	Lys	Ala

200	205	210
Lys Trp Glu Lys Pro Phe His Leu Glu Tyr Thr Arg Lys Asn Phe 215	220	225
Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln Val Pro Met Met 230	235	240
His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn 245	250	255
Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe 260	265	270
Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala 275	280	285
Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys 290	295	300
Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser 305	310	315
Tyr Asn Leu Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala 320	325	330
Phe Asp Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser 335	340	345
Leu Gln Val Ser Lys Ala Thr His Lys Ala Val Leu Asp Val Ser 350	355	360
Glu Glu Gly Thr Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile 365	370	375
Val Arg Ser Lys Asp Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn 380	385	390
Arg Thr Phe Leu Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile 395	400	405
Leu Phe Leu Gly Lys Val Glu Asn Pro Thr Lys Ser 410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 238
ctttgctggtt ggcctctgtg ctccaacca tgcaaggaca ggcgagg 47

<210> 239
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 239
tgactcgggg tctccaaaac cagc 24

<210> 240
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 240
ggtataggcg gaaggcaaag tcgg 24

<210> 241
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 241
ggcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242
<211> 2436
<212> DNA
<213> Homo sapiens

<400> 242
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 cttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta 200
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243
 <211> 596
 <212> PRT
 <213> Homo sapiens

<400> 243
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 20 25 30
 Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala
 35 40 45
 Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala
 50 55 60
 Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val
 65 70 75

Thr Asn Ser Glu Phe His Thr Thr Ser Ser Gly Ile Ser Thr Ala	80	85	90
Thr Asn Ser Glu Phe Ser Thr Ala Ser Ser Gly Ile Ser Ile Ala	95	100	105
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	110	115	120
Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Ser Thr Val	125	130	135
Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Ala Ser Thr Ala	140	145	150
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala	155	160	165
Thr Asn Ser Glu Ser Ser Thr Leu Ser Ser Gly Ala Ser Thr Ala	170	175	180
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	185	190	195
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	200	205	210
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala	215	220	225
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	230	235	240
Thr Asn Ser Glu Ser Arg Thr Thr Ser Asn Gly Ala Gly Thr Ala	245	250	255
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	260	265	270
Thr Asn Ser Asp Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala	275	280	285
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	290	295	300
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	305	310	315
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Gly Thr Ala	320	325	330
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val	335	340	345
Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Asn Thr Ala	350	355	360
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala			

365	370	375
Thr Asn Ser Glu Ser Ser Thr Val Ser	Ser Gly Ala Ser Thr Ala	
380	385	390
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Val Ser Thr Ala	
395	400	405
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr Ala	
410	415	420
Thr Asn Ser Asp Ser Ser Thr Thr Ser	Ser Glu Ala Ser Thr Ala	
425	430	435
Thr Asn Ser Glu Ser Ser Thr Val Ser	Ser Gly Ile Ser Thr Val	
440	445	450
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Asn Thr Ala	
455	460	465
Thr Asn Ser Gly Ser Ser Val Thr Ser	Ala Gly Ser Gly Thr Ala	
470	475	480
Ala Leu Thr Gly Met His Thr Thr Ser	His Ser Ala Ser Thr Ala	
485	490	495
Val Ser Glu Ala Lys Pro Gly Gly Ser	Leu Val Pro Trp Glu Ile	
500	505	510
Phe Leu Ile Thr Leu Val Ser Val Val	Ala Ala Val Gly Leu Phe	
515	520	525
Ala Gly Leu Phe Phe Cys Val Arg Asn	Ser Leu Ser Leu Arg Asn	
530	535	540
Thr Phe Asn Thr Ala Val Tyr His Pro	His Gly Leu Asn His Gly	
545	550	555
Leu Gly Pro Gly Pro Gly Gly Asn His	Gly Ala Pro His Arg Pro	
560	565	570
Arg Trp Ser Pro Asn Trp Phe Trp Arg	Arg Pro Val Ser Ser Ile	
575	580	585
Ala Met Glu Met Ser Gly Arg Asn Ser	Gly Pro	
590	595	

<210> 244

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic sequence.

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 246

ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcatcc 50

ttcccgacct tccagcaat atgcatcttg cacgtctggt cggctcctgc 100

tccctccttc tgctactggg ggccctgtct ggatgggggg ccagcgatga 150

ccccattgag aaggtcattg aagggatcaa ccgagggctg agcaatgcag 200

agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250

gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300

ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350

tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaag 400

gaagcagaga agcttgcca tggggccaac aacgctgctg gacaggccgg 450

gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500

ctgggaagga agcagagaaa cttggccaag gggtaacca tgctgctgac 550

caggctggaa aggaagtgga gaagcttggc caaggtgcc accatgctgc 600

tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650
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 tttctgaaat ccctgaaggg ggttgtactg ggatttgtga ataaacttga 950
 tacacca 957

<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu	
1				5					10					15	
Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	
				20					25					30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	
				35					40					45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	
				50					55					60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	
				65					70					75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	
				80					85					90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	
				95					100					105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	
				110					115					120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	
				125					130					135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	
				140					145					150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	
				155					160					165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	
				170					175					180	

Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser
185 190 195

Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser
200 205 210

Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly
215 220 225

Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
230 235 240

Ser Val Ala Asn Ile Met Pro
245

<210> 249

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 249

caatatgcat cttgcacgtc tgg 23

<210> 250

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 250

aagcttctct gcttcctttc ctgc 24

<210> 251

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 251

tgacccatt gagaaggatc ttgaaggat caaccgaggg ctg 43

<210> 252

<211> 3781

<212> DNA

<213> Homo sapiens

<400> 252

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cagtggacac tccaggaaga gcggccccgc ggggggcat gaccgtgctc 100
tgacctgac tactccagg tccggaggcg ggggcccccg gggcgactcg 150
ggggcggacc gcggggcgga gctgccgcc gtgagtcgg ccgagccacc 200
tgagcccgag ccgcgggaca ccgtcgctcc tgctctccga atgctgcgca 250
ccgcgatggg cctgaggagc tggctcgccg ccccatgggg cgcgctgccg 300
cctcggccac cgctgctgct gtcctgctg ctgctgctcc tgctgcagcc 350
gccgcctccg acctggggcg tcagcccccg gatcagcctg cctctgggct 400
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80

85

90

Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr	
				95					100					105	
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys	
				110					115					120	
Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile	
				125					130					135	
Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	His	Leu	Phe	Thr	Cys	Gly	
				140					145					150	
Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn	
				155					160					165	
Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp	
				170					175					180	
Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	Ser	Thr	Ala	
				185					190					195	
Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe	
				200					205					210	
Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro	
				215					220					225	
Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe	
				230					235					240	
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly	
				245					250					255	
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu	
				260					265					270	
Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile	
				275					280					285	
Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp	
				290					295					300	
Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp	
				305					310					315	
Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro	
				320					325					330	
Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr	
				335					340					345	
Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val	
				350					355					360	
Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys	
				365					370					375	

Glu Val Asn Arg	Glu Thr Gln Gln Trp	Tyr Thr Val Thr His Pro	380	385	390
Val Pro Thr Pro	Arg Pro Gly Ala Cys	Ile Thr Asn Ser Ala Arg	395	400	405
Glu Arg Lys Ile	Asn Ser Ser Leu Gln	Leu Pro Asp Arg Val Leu	410	415	420
Asn Phe Leu Lys	Asp His Phe Leu Met	Asp Gly Gln Val Arg Ser	425	430	435
Arg Met Leu Leu	Leu Gln Pro Gln Ala	Arg Tyr Gln Arg Val Ala	440	445	450
Val His Arg Val	Pro Gly Leu His His	Thr Tyr Asp Val Leu Phe	455	460	465
Leu Gly Thr Gly	Asp Gly Arg Leu His	Lys Ala Val Ser Val Gly	470	475	480
Pro Arg Val His	Ile Ile Glu Glu Leu	Gln Ile Phe Ser Ser Gly	485	490	495
Gln Pro Val Gln	Asn Leu Leu Leu Asp	Thr His Arg Gly Leu Leu	500	505	510
Tyr Ala Ala Ser	His Ser Gly Val Val	Gln Val Pro Met Ala Asn	515	520	525
Cys Ser Leu Tyr	Arg Ser Cys Gly Asp	Cys Leu Leu Ala Arg Asp	530	535	540
Pro Tyr Cys Ala	Trp Ser Gly Ser Ser	Cys Lys His Val Ser Leu	545	550	555
Tyr Gln Pro Gln	Leu Ala Thr Arg Pro	Trp Ile Gln Asp Ile Glu	560	565	570
Gly Ala Ser Ala	Lys Asp Leu Cys Ser	Ala Ser Ser Val Val Ser	575	580	585
Pro Ser Phe Val	Pro Thr Gly Glu Lys	Pro Cys Glu Gln Val Gln	590	595	600
Phe Gln Pro Asn	Thr Val Asn Thr Leu	Ala Cys Pro Leu Leu Ser	605	610	615
Asn Leu Ala Thr	Arg Leu Trp Leu Arg	Asn Gly Ala Pro Val Asn	620	625	630
Ala Ser Ala Ser	Cys His Val Leu Pro	Thr Gly Asp Leu Leu Leu	635	640	645
Val Gly Thr Gln	Gln Leu Gly Glu Phe	Gln Cys Trp Ser Leu Glu	650	655	660
Glu Gly Phe Gln	Gln Leu Val Ala Ser	Tyr Cys Pro Glu Val Val			

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665	670	675
Glu Asp Gly Val Ala Asp Gln Thr Asp	Glu Gly Gly Ser Val Pro	
680	685	690
Val Ile Ile Ser Thr Ser Arg Val Ser	Ala Pro Ala Gly Gly Lys	
695	700	705
Ala Ser Trp Gly Ala Asp Arg Ser Tyr	Trp Lys Glu Phe Leu Val	
710	715	720
Met Cys Thr Leu Phe Val Leu Ala Val	Leu Leu Pro Val Leu Phe	
725	730	735
Leu Leu Tyr Arg His Arg Asn Ser Met	Lys Val Phe Leu Lys Gln	
740	745	750
Gly Glu Cys Ala Ser Val His Pro Lys	Thr Cys Pro Val Val Leu	
755	760	765
Pro Pro Glu Thr Arg Pro Leu Asn Gly	Leu Gly Pro Pro Ser Thr	
770	775	780
Pro Leu Asp His Arg Gly Tyr Gln Ser	Leu Ser Asp Ser Pro Pro	
785	790	795
Gly Ala Arg Val Phe Thr Glu Ser Glu	Lys Arg Pro Leu Ser Ile	
800	805	810
Gln Asp Ser Phe Val Glu Val Ser Pro	Val Cys Pro Arg Pro Arg	
815	820	825
Val Arg Leu Gly Ser Glu Ile Arg Asp	Ser Val Val	
830	835	

<210> 254
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 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 254
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 <210> 255
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 255
tgaagccagg gcagcgtcct ctgg 24

<210> 256
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 256
gtacaggctg cagttggc 18

<210> 257
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 257
agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258
<211> 45
<212> DNA
<213> Artificial

<220>
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<222> 1-45
<223> Synthetic construct.

<400> 258
gagctgcaga tcttctcatc gggacagccc gtgcagaatc tgctc 45

<210> 259
<211> 4563
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 3635
<223> unknown base

<400> 259
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cggggacagg cgccgtgcga accgagccca gccagccgga ggacgcgggc 100

agggcgggac gggagcccgg actcgtctgc cgccgccgtc gtcgccgtcg 150

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 gtatttacag cagactttca gcaaatcca gtttgtggag catgaggagc 1950
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<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro
35 40 45

Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly
50 55 60

Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser
65 70 75

Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly
80 85 90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala
95 100 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe
110 115 120

Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro
125 130 135

Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
140 145 150

Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu
155 160 165

Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg
170 175 180

Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe
185 190 195

Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu
200 205 210

Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val
215 220 225

Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
230 235 240

Lys Cys Leu Arg	Glu Met Tyr Thr Thr	His Glu Asp Val Glu Val	245	250	255
Gly Arg Cys Val	Arg Arg Phe Ala Gly	Val Gln Cys Val Trp Ser	260	265	270
Tyr Glu Met Arg	Gln Leu Phe Tyr Glu	Asn Tyr Glu Gln Asn Lys	275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn	Ser Lys Ile His Gln Ala	290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro	Pro Tyr Gln Tyr Arg Leu	305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile	Ser Glu Leu Arg His Arg	320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val	Leu Met Ser Lys Tyr Ser	335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu	Gln Leu Gly Ile Pro Pro	350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln	Arg Glu Glu Ile Leu Glu	365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu	Tyr Ser Ala Val Asp Gly	380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser	Ala Gln Arg Glu Ala Leu	395	400	405
Asp Asp Ile Val	Met Gln Val Met Glu	Met Ile Asn Ala Asn Ala	410	415	420
Lys Thr Arg Gly	Arg Ile Ile Asp Phe	Lys Glu Ile Gln Tyr Gly	425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly	Ala Glu Tyr Ile Leu Asp	440	445	450
Leu Leu Leu Leu	Tyr Lys Lys His Lys	Gly Lys Lys Met Thr Val	455	460	465
Pro Val Arg Arg	His Ala Tyr Leu Gln	Gln Thr Phe Ser Lys Ile	470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp	Ala Gln Glu Leu Ala Lys	485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu	Ser Phe Leu Ser Asn Ser	500	505	510
Leu Lys Lys Leu	Val Pro Phe Gln Leu	Pro Gly Ser Lys Ser Glu	515	520	525
His Lys Glu Pro	Lys Asp Lys Lys Ile	Asn Ile Leu Ile Pro Leu			

530	535	540
Ser Gly Arg Phe Asp Met Phe Val Arg	Phe Met Gly Asn Phe	Glu
545	550	555
Lys Thr Cys Leu Ile Pro Asn Gln Asn	Val Lys Leu Val Val	Leu
560	565	570
Leu Phe Asn Ser Asp Ser Asn Pro Asp	Lys Ala Lys Gln Val	Glu
575	580	585
Leu Met Arg Asp Tyr Arg Ile Lys Tyr	Pro Lys Ala Asp Met	Gln
590	595	600
Ile Leu Pro Val Ser Gly Glu Phe Ser	Arg Ala Leu Ala Leu	Glu
605	610	615
Val Gly Ser Ser Gln Phe Asn Asn Glu	Ser Leu Leu Phe Phe	Cys
620	625	630
Asp Val Asp Leu Val Phe Thr Thr Glu	Phe Leu Gln Arg Cys	Arg
635	640	645
Ala Asn Thr Val Leu Gly Gln Gln Ile	Tyr Phe Pro Ile Ile	Phe
650	655	660
Ser Gln Tyr Asp Pro Lys Ile Val Tyr	Ser Gly Lys Val Pro	Ser
665	670	675
Asp Asn His Phe Ala Phe Thr Gln Lys	Thr Gly Phe Trp Arg	Asn
680	685	690
Tyr Gly Phe Gly Ile Thr Cys Ile Tyr	Lys Gly Asp Leu Val	Arg
695	700	705
Val Gly Gly Phe Asp Val Ser Ile Gln	Gly Trp Gly Leu Glu	Asp
710	715	720
Val Asp Leu Phe Asn Lys Val Val Gln	Ala Gly Leu Lys Thr	Phe
725	730	735
Arg Ser Gln Glu Val Gly Val Val His	Val His His Pro Val	Phe
740	745	750
Cys Asp Pro Asn Leu Asp Pro Lys Gln	Tyr Lys Met Cys Leu	Gly
755	760	765
Ser Lys Ala Ser Thr Tyr Gly Ser Thr	Gln Gln Leu Ala Glu	Met
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<210> 261

<211> 24

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 <220>
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 <222> 1-24
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 <400> 261
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 <211> 24
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-24
 <223> Synthetic construct.

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<210> 263
 <211> 46
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 <213> Artificial

<220>
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 <223> Synthetic construct.

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<210> 264
 <211> 1419
 <212> DNA
 <213> Homo sapiens

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 tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

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<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

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Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20				25					30	

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35				40					45	

Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	50	55	60
Pro Lys His Val Tyr Ser Ile Ala Ser Lys Gly Ser Lys Phe Lys	65	70	75
Glu Leu Val Thr His Gly Asp Ala Ser Thr Glu Asn Asp Val Leu	80	85	90
Thr Asn Pro Ile Ser Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly	95	100	105
Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro	110	115	120
Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala	125	130	135
Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu	140	145	150
Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val	155	160	165
Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro	170	175	180
Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu	185	190	195
Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys	200	205	210
Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp	215	220	225
Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala	230	235	240
Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu	245	250	255
Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala	260	265	270
Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro	275	280	285
Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile	290	295	300
Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp	305	310	315
Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val	320	325	330
Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala	335	340	345

Leu Leu Lys Val Tyr
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<210> 266

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 266

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<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

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Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

	20	25	30
Leu Val Gly Glu Asp	Ala Val Phe Ser Cys	Ser Leu Phe Pro	Glu
	35	40	45
Thr Ser Ala Glu Ala	Met Glu Val Arg Phe	Phe Arg Asn Gln	Phe
	50	55	60
His Ala Val Val His	Leu Tyr Arg Asp Gly	Glu Asp Trp Glu	Ser
	65	70	75
Lys Gln Met Pro Gln	Tyr Arg Gly Arg Thr	Glu Phe Val Lys	Asp
	80	85	90
Ser Ile Ala Gly Gly	Arg Val Ser Leu Arg	Leu Lys Asn Ile	Thr
	95	100	105
Pro Ser Asp Ile Gly	Leu Tyr Gly Cys Trp	Phe Ser Ser Gln	Ile
	110	115	120
Tyr Asp Glu Glu Ala	Thr Trp Glu Leu Arg	Val Ala Ala Leu	Gly
	125	130	135
Ser Leu Pro Leu Ile	Ser Ile Val Gly Tyr	Val Asp Gly Gly	Ile
	140	145	150
Gln Leu Leu Cys Leu	Ser Ser Gly Trp Phe	Pro Gln Pro Thr	Ala
	155	160	165
Lys Trp Lys Gly Pro	Gln Gly Gln Asp Leu	Ser Ser Asp Ser	Arg
	170	175	180
Ala Asn Ala Asp Gly	Tyr Ser Leu Tyr Asp	Val Glu Ile Ser	Ile
	185	190	195
Ile Val Gln Glu Asn	Ala Gly Ser Ile Leu	Cys Ser Ile His	Leu
	200	205	210
Ala Glu Gln Ser His	Glu Val Glu Ser Lys	Val Leu Ile Gly	Glu
	215	220	225
Thr Phe Phe Gln Pro	Ser Pro Trp Arg Leu	Ala Ser Ile Leu	Leu
	230	235	240
Gly Leu Leu Cys Gly	Ala Leu Cys Gly Val	Val Met Gly Met	Ile
	245	250	255
Ile Val Phe Phe Lys	Ser Lys Gly Lys Ile	Gln Ala Glu Leu	Asp
	260	265	270
Trp Arg Arg Lys His	Gly Gln Ala Glu Leu	Arg Asp Ala Arg	Lys
	275	280	285
His Ala Val Glu Val	Thr Leu Asp Pro Glu	Thr Ala His Pro	Lys
	290	295	300
Leu Cys Val Ser Asp	Leu Lys Thr Val Thr	His Arg Lys Ala	Pro
	305	310	315

Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val	320	325	330
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val	335	340	345
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp	350	355	360
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn	365	370	375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr	380	385	390
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr	395	400	405
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe	410	415	420
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys	425	430	435
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr	440	445	450
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp	455	460	465

Gly

<210> 268
 <211> 2103
 <212> DNA
 <213> Homo sapiens

<400> 268

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 tgccagatgg actgcttctt ttggagtaac aataaaacct tcgaaaatga 800
 aacgggggtct ccggagaata attgtccatg aaaaatacaa acacccatca 850
 catgactatg atatttctct tgcagagctt tctagccctg ttccctacac 900
 aaatgcagta catagagttt gtctccctga tgcctcctat gagtttcaac 950
 caggatgatgt gatgtttgtg acaggatttg gagcactgaa aaatgatggt 1000
 tacagtcaaa atcatcttctg acaagcacag gtgactctca tagacgctac 1050
 aacttgcaat gaacctcaag cttacaatga cgccataact cctagaatgt 1100
 tatgtgctgg ctcccttagaa ggaaaaacag atgcatgcca ggggtgactct 1150
 ggaggaccac tgggttagttc agatgctaga gatattctggt accttgctgg 1200
 aatagtgage tggggagatg aatgtgcgaa acccaacaag cctgggtgttt 1250
 atactagagt tacggccttg cgggactgga ttacttcaaa aactggtatc 1300
 taagagacaa aagcctcatg gaacagataa catttttttt tgtttttttg 1350
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 gctagatttg actgatctca ataaactggt tgcttgatgc atgtattttc 1450
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 cagaattttg acttggtgac ataaatttgt aatgcatata tacaatttga 1650
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 aatattagaa atgatcatat tcattatgaa aggtcaagca aagacagcag 1850
 aataccaatc acttcatcat ttaggaagta tgggaactaa gttaaggaag 1900
 tccagaaaga agccaagata tatccttatt ttcatttcca aacaactact 1950

atgataaatg tgaagaagat tctgtttttt tgtgacctat aataattata 2000
 caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatttat 2050
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 cca 2103

<210> 269
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 269

Met	Met	Tyr	Arg	Pro	Asp	Val	Val	Arg	Ala	Arg	Lys	Arg	Val	Cys	1	5	10	15
Trp	Glu	Pro	Trp	Val	Ile	Gly	Leu	Val	Ile	Phe	Ile	Ser	Leu	Ile	20	25	30	
Val	Leu	Ala	Val	Cys	Ile	Gly	Leu	Thr	Val	His	Tyr	Val	Arg	Tyr	35	40	45	
Asn	Gln	Lys	Lys	Thr	Tyr	Asn	Tyr	Tyr	Ser	Thr	Leu	Ser	Phe	Thr	50	55	60	
Thr	Asp	Lys	Leu	Tyr	Ala	Glu	Phe	Gly	Arg	Glu	Ala	Ser	Asn	Asn	65	70	75	
Phe	Thr	Glu	Met	Ser	Gln	Arg	Leu	Glu	Ser	Met	Val	Lys	Asn	Ala	80	85	90	
Phe	Tyr	Lys	Ser	Pro	Leu	Arg	Glu	Glu	Phe	Val	Lys	Ser	Gln	Val	95	100	105	
Ile	Lys	Phe	Ser	Gln	Gln	Lys	His	Gly	Val	Leu	Ala	His	Met	Leu	110	115	120	
Leu	Ile	Cys	Arg	Phe	His	Ser	Thr	Glu	Asp	Pro	Glu	Thr	Val	Asp	125	130	135	
Lys	Ile	Val	Gln	Leu	Val	Leu	His	Glu	Lys	Leu	Gln	Asp	Ala	Val	140	145	150	
Gly	Pro	Pro	Lys	Val	Asp	Pro	His	Ser	Val	Lys	Ile	Lys	Lys	Ile	155	160	165	
Asn	Lys	Thr	Glu	Thr	Asp	Ser	Tyr	Leu	Asn	His	Cys	Cys	Gly	Thr	170	175	180	
Arg	Arg	Ser	Lys	Thr	Leu	Gly	Gln	Ser	Leu	Arg	Ile	Val	Gly	Gly	185	190	195	
Thr	Glu	Val	Glu	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	200	205	210	
Trp	Asp	Gly	Ser	His	Arg	Cys	Gly	Ala	Thr	Leu	Ile	Asn	Ala	Thr	215	220	225	

Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro	
				230					235					240	
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys	
				245					250					255	
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys	
				260					265					270	
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser	
				275					280					285	
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp	
				290					295					300	
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly	
				305					310					315	
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg	
				320					325					330	
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro	
				335					340					345	
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly	
				350					355					360	
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	
				365					370					375	
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly	
				380					385					390	
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly	
				395					400					405	
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys	
				410					415					420	

Thr Gly Ile

<210> 270
 <211> 1170
 <212> DNA
 <213> Homo sapiens

<400> 270
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 aacctgacag cacagcctga gatcttgggg atccctcagc ctaacaccca 100
 cagacgtcag ctggtggatt cccgctgcat caaggcctac ccactgtctc 150
 catgctgggc tctccctgcc ttctgtggct cctggccgtg accttcttgg 200
 ttcccagagc tcagcccttg gccctcaag actttgaaga agaggaggca 250

gatgagactg agacggcgtg gccgcctttg ccggctgtcc cctgcgacta 300
cgaccactgc cgacacctgc aggtgccctg caaggagcta cagagggtcg 350
ggccggcggc ctgcctgtgc ccaggactct ccagccccgc ccagccgccc 400
gacccgcccgc gcatgggaga agtgcgcatc gcggccgaag agggccgcgc 450
agtgggtccac tgggtgtgcc ccttctcccc ggtcctccac tactggctgc 500
tgctttggga cggcagcgag gctgcgcaga aggggcccc gctgaacgct 550
acggtccgca gagccgaact gaaggggctg aagccagggg gcatttatgt 600
cgtttgcgta gtggccgcta acgaggccgg ggcaagccgc gtgccccagg 650
ctggaggaga gggcctcgag ggggccgaca tccctgcctt cgggccttgc 700
agccgccttg cggtgccgcc caacccccgc actctgggtcc acgcggccgt 750
cgggggtgggc acggccctgg ccttgctaag ctgtgccgcc ctgggtgtggc 800
acttctgcct gcgcgatcgc tggggctgcc cgcgccgagc cgcgcgccga 850
gccgcagggg cgctctgaaa ggggcctggg ggcatctcgg gcacagacag 900
ccccacctgg ggcgctcagc ctggcccccg ggaaagagga aaacccgctg 950
cctccaggga gggctggacg gcgagctggg agccagcccc aggctccagg 1000
gccacggcgg agtcatggtt ctcaggactg agcgcttggt taggtccggt 1050
acttggcgct ttgtttcctg gctgaggtct gggaaggaat agaaaggggc 1100
ccccaatttt tttttaagcg gccagataat aaataatgta acctttgcgg 1150
ttaaaaaaaaa aaaaaaaaaa 1170

<210> 271
<211> 238
<212> PRT
<213> Homo sapiens

<400> 271
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1 5 10 15
Leu Val Pro Arg Ala Gln Pro Leu Ala Pro Gln Asp Phe Glu Glu
20 25 30
Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala
35 40 45
Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys
50 55 60
Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly
65 70 75

Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	80	85	90
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	95	100	105
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	110	115	120
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	125	130	135
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	140	145	150
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	155	160	165
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	170	175	180
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	185	190	195
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	200	205	210
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	215	220	225
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			230	235	

<210> 272
 <211> 2397
 <212> DNA
 <213> Homo sapiens

<400> 272
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 cccaggcggg cgtggggcac cgggccagc gccgacgatc gctgccgttt 150
 tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200
 gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgcctgctct 250
 acgccctcaa tctgctcttt tggtaaatgt ccatcagtgt gttggcagtt 300
 tctgcttggg tgagggacta cctaaataat gttctcactt taactgcaga 350
 aacgagggta gaggaagcag tcattttgac ttaacttcct gtggttcac 400
 cggatcatgat tgctgtttgc tgtttcotta tcattgtggg gatgttagga 450
 tattgtggaa cggtgaaaag aaatctgttg cttcttgcat ggtactttgg 500

agaatgtagt ctggtcttta ggaagtatta ataagaaaat ttgcacataa 2000
 cttagttgat tcagaaagga cttgtatgct gtttttctcc caaatgaaga 2050
 ctctttttga cactaaacac tttttaaaaa gcttatcttt gccttctcca 2100
 aacaagaagc aatagtctcc aagtcaatat aaattctaca gaaaatagtg 2150
 ttctttttct ccagaaaaat gcttgtgaga atcattaaaa catgtgacaa 2200
 tttagagatt ctttgtttta tttcactgat taatatactg tggcaaatta 2250
 cacagattat taaatttttt tacaagagta tagtatattt atttgaaatg 2300
 ggaaaagtgc attttactgt attttgtgta ttttgtttat ttctcagaat 2350
 atggaaagaa aattaaaatg tgtcaataaa tattttctag agagtaa 2397

<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

Met	Ala	Arg	Glu	Asp	Ser	Val	Lys	Cys	Leu	Arg	Cys	Leu	Leu	Tyr
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Ala	Leu	Asn	Leu	Leu	Phe	Trp	Leu	Met	Ser	Ile	Ser	Val	Leu	Ala
				20					25					30
Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu
				35					40					45
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe
				50					55					60
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile
				65					70					75
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu
				80					85					90
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys
				95					100					105
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met
				110					115					120
Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met
				125					130					135
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp
				140					145					150
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe
				155					160					165
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser

170	175	180
Cys Cys Val Arg Glu Phe Pro Gly Cys Ser Lys Gln Ala His Gln		
185	190	195
Glu Asp Leu Ser Asp Leu Tyr Gln Glu Gly Cys Gly Lys Lys Met		
200	205	210
Tyr Ser Phe Leu Arg Gly Thr Lys Gln Leu Gln Val Leu Arg Phe		
215	220	225
Leu Gly Ile Ser Ile Gly Val Thr Gln Ile Leu Ala Met Ile Leu		
230	235	240
Thr Ile Thr Leu Leu Trp Ala Leu Tyr Tyr Asp Arg Arg Glu Pro		
245	250	255
Gly Thr Asp Gln Met Met Ser Leu Lys Asn Asp Asn Ser Gln His		
260	265	270
Leu Ser Cys Pro Ser Val Glu Leu Leu Lys Pro Ser Leu Ser Arg		
275	280	285
Ile Phe Glu His Thr Ser Met Ala Asn Ser Phe Asn Thr His Phe		
290	295	300
Glu Met Glu Glu Leu		
305		

<210> 274

<211> 2063

<212> DNA

<213> Homo sapiens

<400> 274

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agagccagca tgttacagga tcttgacagt gatcaacctc tgaacagcct 250

cgatgtcaaa cccctgcga aaccccgat ccccatggag accttcagaa 300

aggtggggat ccccatcatc atagcactac tgagcctggc gagtatcatc 350

attgtggttg tctcatcaa ggtgattctg gataaatact acttcctctg 400

cgggcagcct ctccacttca tcccaggaa gcagctgtgt gacggagagc 450

tggactgtcc cttgggggag gacgaggagc actgtgtcaa gagcttcccc 500

gaagggcctg cagtggcagt ccgcctctcc aaggaccgat ccacactgca 550

ggtgctggac tcggccacag ggaactggtt ctctgcctgt ttcgacaact 600

tcacagaagc tctcgtgag acagcctgta ggcagatggg ctacagcaga 650
 gctgtggaga ttggcccaga ccaggatctg gatgttggtg aaatcacaga 700
 aaacagccag gagcttcgca tgcggaactc aagtgggccc tgtctctcag 750
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 gagggaagat gtctgacata ctgctgcagg cgtcagtcca ggtcattgac 1250
 agcacacggt gcaatgcaga cgatgcgtac cagggggaag tcaccgagaa 1300
 gatgatgtgt gcaggcatcc cggaaggggg tgtggacacc tgccagggtg 1350
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 caccaaggtc tcagcctatc tcaactggat ctacaatgtc tggaaggctg 1500
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 ttgggtacac ccctctgccc acagcctcag catttcttg agcagcaaag 1650
 ggcctcaatt cctgtaagag accctcgag cccagaggcg cccagaggaa 1700
 gtcagcagcc ctagctcggc cacacttggt gctcccagca tcccaggag 1750
 agacacagcc cactgaacaa ggtctcagg gtattgctaa gccaagaagg 1800
 aactttccca cactactgaa tggaagcagg ctgtcttgta aaagcccaga 1850
 tcaactgtgg ctggagagga gaaggaaagg gtctgcgcca gccctgtccg 1900
 tcttcacca tccccagcc tactagagca agaaaccagt tgtaataata 1950
 aatgcactgc cctactgttg gtatgactac cgttacctac tgttgtcatt 2000
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caaaaaaaaaaaa aaa 2063

<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

Met	Leu	Gln	Asp	Pro	Asp	Ser	Asp	Gln	Pro	Leu	Asn	Ser	Leu	Asp	
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Val	Lys	Pro	Leu	Arg	Lys	Pro	Arg	Ile	Pro	Met	Glu	Thr	Phe	Arg	
				20					25					30	
Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser	
				35					40					45	
Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr	
				50					55					60	
Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln	
				65					70					75	
Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu	
				80					85					90	
His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg	
				95					100					105	
Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr	
				110					115					120	
Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu	
				125					130					135	
Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu	
				140					145					150	
Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn	
				155					160					165	
Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser	
				170					175					180	
Gly	Ser	Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu	
				185					190					195	
Lys	Thr	Pro	Arg	Val	Val	Gly	Gly	Glu	Glu	Ala	Ser	Val	Asp	Ser	
				200					205					210	
Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr	Asp	Lys	Gln	His	Val	Cys	
				215					220					225	
Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His	
				230					235					240	
Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala	
				245					250					255	

Gly Ser Asp Lys Leu Gly Ser Phe Pro	Ser Leu Ala Val Ala Lys
260	265 270
Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp Asn Asp	
275	280 285
Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly Thr	
290	295 300
Val Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro	
305	310 315
Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn	
320	325 330
Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val	
335	340 345
Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu	
350	355 360
Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val	
365	370 375
Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser	
380	385 390
Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys	
395	400 405
Gly Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr	
410	415 420
Leu Asn Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu	
425	430

<210> 276
 <211> 3143
 <212> DNA
 <213> Homo sapiens

<400> 276
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 ggaggcgggc aggggcccac gccaggggtc agatactatg caggggatga 250
 acgtagggca cttagcttct tccaccagaa gggcctccag gattttgaca 300
 ctctgctcct gagtggatgat ggaaatactc tctacgtggg ggctcgagaa 350
 gccattctgg ccttgatat ccaggatcca ggggtcccca ggctaaagaa 400

catgataccg tggccagcca gtgacagaaa aaagagtga tgtgccttta 450
agaagaagag caatgagaca cagtgtttca acttcatccg tgtcctgggt 500
tcttacaatg tcacccatct ctacacctgc ggcaccttcg ccttcagccc 550
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caacttctcg ggcagtgagc ccatcctgat gcgcacactg ggatcccagc 750
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gacagccagc gagtttgact tctttgagag gctccacaca tcgcgggtgg 900
ctagagtctg caagaatgac gtgggcggcg aaaagctgct gcagaagaag 950
tggaccacct tcctgaaggc ccagctgctc tgcaccagc cggggcagct 1000
gcccttcaac gtcacccgcc acgcggctct gctccccgcc gattctccca 1050
cagctcccca catctacgca gtcttcacct cccagtggca ggttggcggg 1100
accaggagct ctgcggtttg tgccttctct ctcttggaca ttgaacgtgt 1150
ctttaagggg aaatacaaag agttgaacaa agaaacttca cgctggacta 1200
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ccctcctctg ataaggccct gaccttcatg aaggaccatt tcctgatgga 1300
tgagcaagtg gtggggagcg ccctgctggt gaaatctggc gtggagtata 1350
cacggcttgc agtgagagca gcccagggcc ttgatgggca cagccatctt 1400
gtcatgtacc tgggaaccac cacagggtcg ctccacaagg ctgtggtaag 1450
tggggacagc agtgctcatc tgggtgaaga gattcagctg ttccctgacc 1500
ctgaacctgt tcgcaacctg cagctggccc ccaccaggg tgcagtgttt 1550
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 agaagcctct tccactgtct acaatggctc cctcttgctg atagtgcagg 1950
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<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

Met Ala Leu Pro Ala Leu Gly Leu Asp Pro Trp Ser Leu Leu Gly
 1 5 10 15
 Leu Phe Leu Phe Gln Leu Leu Gln Leu Leu Leu Pro Thr Thr Thr
 20 25 30
 Ala Gly Gly Gly Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Tyr
 35 40 45
 Ala Gly Asp Glu Arg Arg Ala Leu Ser Phe Phe His Gln Lys Gly
 50 55 60
 Leu Gln Asp Phe Asp Thr Leu Leu Leu Ser Gly Asp Gly Asn Thr
 65 70 75
 Leu Tyr Val Gly Ala Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln
 80 85 90
 Asp Pro Gly Val Pro Arg Leu Lys Asn Met Ile Pro Trp Pro Ala
 95 100 105
 Ser Asp Arg Lys Lys Ser Glu Cys Ala Phe Lys Lys Lys Ser Asn
 110 115 120
 Glu Thr Gln Cys Phe Asn Phe Ile Arg Val Leu Val Ser Tyr Asn
 125 130 135
 Val Thr His Leu Tyr Thr Cys Gly Thr Phe Ala Phe Ser Pro Ala
 140 145 150
 Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr Leu Leu Pro Ile Ser
 155 160 165
 Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser Pro Phe Asp Pro
 170 175 180
 Ala His Lys His Thr Ala Val Leu Val Asp Gly Met Leu Tyr Ser
 185 190 195
 Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu Met Arg
 200 205 210
 Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu Arg
 215 220 225
 Trp Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr
 230 235 240
 Gln Val Val Tyr Phe Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp
 245 250 255
 Phe Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys
 260 265 270
 Asn Asp Val Gly Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Thr
 275 280 285
 Phe Leu Lys Ala Gln Leu Leu Cys Thr Gln Pro Gly Gln Leu Pro

290	295	300
Phe Asn Val Ile Arg His Ala Val Leu	Leu Pro Ala Asp Ser Pro	
305	310	315
Thr Ala Pro His Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln Val	
320	325	330
Gly Gly Thr Arg Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu Asp	
335	340	345
Ile Glu Arg Val Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys Glu	
350	355	360
Thr Ser Arg Trp Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro Arg	
365	370	375
Pro Gly Ser Cys Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu Thr	
380	385	390
Phe Met Lys Asp His Phe Leu Met Asp	Glu Gln Val Val Gly Thr	
395	400	405
Pro Leu Leu Val Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala Val	
410	415	420
Glu Thr Ala Gln Gly Leu Asp Gly His	Ser His Leu Val Met Tyr	
425	430	435
Leu Gly Thr Thr Thr Gly Ser Leu His	Lys Ala Val Val Ser Gly	
440	445	450
Asp Ser Ser Ala His Leu Val Glu Glu	Ile Gln Leu Phe Pro Asp	
455	460	465
Pro Glu Pro Val Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly Ala	
470	475	480
Val Phe Val Gly Phe Ser Gly Gly Val	Trp Arg Val Pro Arg Ala	
485	490	495
Asn Cys Ser Val Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala Arg	
500	505	510
Asp Pro His Cys Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys Leu	
515	520	525
Leu Ser Ala Pro Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu Arg	
530	535	540
Gly Asn Pro Glu Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg Ser	
545	550	555
Leu Arg Pro Gln Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu Ala	
560	565	570
Val Pro Asn Ser Ile Leu Glu Leu Pro	Cys Pro His Leu Ser Ala	
575	580	585

Leu	Ala	Ser	Tyr	Tyr	Trp	Ser	His	Gly	Pro	Ala	Ala	Val	Pro	Glu	590	595	600
Ala	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Ser	Leu	Leu	Leu	Ile	Val	Gln	605	610	615
Asp	Gly	Val	Gly	Gly	Leu	Tyr	Gln	Cys	Trp	Ala	Thr	Glu	Asn	Gly	620	625	630
Phe	Ser	Tyr	Pro	Val	Ile	Ser	Tyr	Trp	Val	Asp	Ser	Gln	Asp	Gln	635	640	645
Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu	His	650	655	660
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu	Ala	665	670	675
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val	Leu	680	685	690
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala	Ser	695	700	705
Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys	Glu	710	715	720
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln	His	725	730	735
Leu	Gln	Ser	Pro	Lys	Glu	Cys	Arg	Thr	Ser	Ala	Ser	Asp	Val	Asp	740	745	750
Ala	Asp	Asn	Asn	Cys	Leu	Gly	Thr	Glu	Val	Ala					755	760	

<210> 278
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 278
 ctgctggtga aatctggcgt ggag 24

<210> 279
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 279
gtctggtcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 280
catcttgtca tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
aggggtccctt agccggggcgc agggcgcgca gccagggctg agatccgcgg 50
cttccgtaga agtgagcatg gctgggcagc gagtgcttct tctagtgggc 100
ttccttctcc ctgggggtcct gctctcagag gctgccaaaa tcttgacaat 150
atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200
ttcttcaaga tcacgggtcat aatgtcacca tgcttaacca caaaagaggt 250
ccttttatgc cagattttta aaaggaagaa aaatcatatc aagttatcag 300
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450
ggatatcatg gattccttaa agaatgagaa cttcgacatg gtgatagttg 500
aaacttttga ctactgtcct ttcttgattg ctgagaagct tgggaagcca 550
tttgtggcca ttctttccac ttcatcggc tctttggaat ttgggctacc 600
aatccccttg tottatgttc cagtattccg ttccttgctg actgatcaca 650
tggacttctg gggccgagtg aagaattttc tgatgttctt tagtttctgc 700
aggaggcaac agcacatgca gtctacattt gacaacacca tcaaggaaca 750
tttcacagaa ggctctaggc cagttttgtc tcatcttcta ctgaaagcag 800
agttgtgggtt cattaactct gactttgcct ttgattttgc tcgacctctg 850
cttcccaaca ctgtttatgt tggaggcttg atggaaaaac ctattaaacc 900

agtaccacaa gacttggaga acttcattgc caagtttggg gactctgggt 950
 ttgtccttgt gaccttgggc tccatggtga acacctgtca gaatccggaa 1000
 atcttcaagg agatgaacaa tgcctttgct cacctacccc aaggggtgat 1050
 atggaagtgt cagtgttctc attggcccaa agatgtccac ctggctgcaa 1100
 atgtgaaaat tgtggactgg ctctctcaga gtgacctcct ggctcaccca 1150
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 atctatcatg gaataacatc caagaaagac accttgcata ttctttcagt 2100
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 tgtgcttgag agttcagggc cggacacagg ctcacaggtc tccacattgg 2200
 gtccctgtct ctggtgcccc cagtgagctc cttcttggct gagcaggcat 2250
 ggagactgta ggtttccaga tttcctgaaa aataaaagt ttacagcgta 2300
 totctcccca acctcactaa 2320

<210> 282
 <211> 523
 <212> PRT
 <213> Homo sapiens

<400> 282

Met	Ala	Gly	Gln	Arg	Val	Leu	Leu	Leu	Val	Gly	Phe	Leu	Leu	Pro	1	5	10	15
Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr	20	25	30	
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile	35	40	45	
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg	50	55	60	
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln	65	70	75	
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys	80	85	90	
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly	95	100	105	
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln	110	115	120	
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys	125	130	135	
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys	140	145	150	
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile	155	160	165	
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro	170	175	180	
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met	185	190	195	
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe	200	205	210	
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile	215	220	225	
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu	230	235	240	
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe	245	250	255	
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly				

260	265	270
Leu Met Glu Lys Pro Ile Lys Pro Val	Pro Gln Asp Leu Glu Asn	
275	280	285
Phe Ile Ala Lys Phe Gly Asp Ser Gly	Phe Val Leu Val Thr Leu	
290	295	300
Gly Ser Met Val Asn Thr Cys Gln Asn	Pro Glu Ile Phe Lys Glu	
305	310	315
Met Asn Asn Ala Phe Ala His Leu Pro	Gln Gly Val Ile Trp Lys	
320	325	330
Cys Gln Cys Ser His Trp Pro Lys Asp	Val His Leu Ala Ala Asn	
335	340	345
Val Lys Ile Val Asp Trp Leu Pro Gln	Ser Asp Leu Leu Ala His	
350	355	360
Pro Ser Ile Arg Leu Phe Val Thr His	Gly Gly Gln Asn Ser Ile	
365	370	375
Met Glu Ala Ile Gln His Gly Val Pro	Met Val Gly Ile Pro Leu	
380	385	390
Phe Gly Asp Gln Pro Glu Asn Met Val	Arg Val Glu Ala Lys Lys	
395	400	405
Phe Gly Val Ser Ile Gln Leu Lys Lys	Leu Lys Ala Glu Thr Leu	
410	415	420
Ala Leu Lys Met Lys Gln Ile Met Glu	Asp Lys Arg Tyr Lys Ser	
425	430	435
Ala Ala Val Ala Ala Ser Val Ile Leu	Arg Ser His Pro Leu Ser	
440	445	450
Pro Thr Gln Arg Leu Val Gly Trp Ile	Asp His Val Leu Gln Thr	
455	460	465
Gly Gly Ala Thr His Leu Lys Pro Tyr	Val Phe Gln Gln Pro Trp	
470	475	480
His Glu Gln Tyr Leu Phe Asp Val Phe	Val Phe Leu Leu Gly Leu	
485	490	495
Thr Leu Gly Thr Leu Trp Leu Cys Gly	Lys Leu Leu Gly Met Ala	
500	505	510
Val Trp Trp Leu Arg Gly Ala Arg Lys	Val Lys Glu Thr	
515	520	

<210> 283
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 283
 tgcctttgct cacctacccc aagg 24

<210> 284
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 284
 tcaggctggt ctccaaagag aggg 24

<210> 285
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 285
 cccaaagatg tccacctggc tgcaaagtgtg aaaattgtgg actgg 45

<210> 286
 <211> 2340
 <212> DNA
 <213> Homo sapiens

<400> 286
 gggctgttga tttgtggggg attttgaaga gaggaggaat aggaggaagg 50
 gggtgagggg ctgcctcttg catatgcaca cactcacaca ttctgtcaca 100
 cccgtcacac acacatacca tgttctccat cccccaggt ccagccctca 150
 gtgctgtccc atccagcagg gctaccctga agctctgggt gcagccctcc 200
 cgtccagtgg gcaggcggct tcatccctcc tttctctccc aaagcccaac 250
 tgctgtcact gcatgctctg ccaaggagga gggaactgca gtgacagcag 300
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 gttcagcgag cctagagagg gcagactatc agggtgccgg cggtgagaat 400
 ccagggagag gagcggaac agaagagggg cagaagaccg gggcacttgt 450

gggttgcaga gccctcagc catgttggga gccaagccac actggtacc 500
 aggtccccta cacagtcccg ggctgccctt ggttctggtg cttctggccc 550
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 gggagcagcc ctgggagagg caccocctgg gcgagtggca ttgtctgagg 700
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 ccgggcctct ggctccttcg tagccctgt ccgggggtgtc tacagcttcc 850
 ggttccatgt ggtgaagggtg tacaaccgcc aaactgtcca ggtgagcctg 900
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 gaccggggag gcagccacca gctctgtgct actgcccttg gaccctgggg 1000
 accgagtgtc tctgcgcctg cgtcggggga atctactggg tggttggaaa 1050
 tactcaagtt tctctggctt cctcatcttc cctctctgag gacccaagtc 1100
 tttcaagcac aagaatccag cccctgacaa ctttcttctg ccctctcttg 1150
 cccagaaac agcagaggca ggagagagac tccctctggc tcctatccca 1200
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 ccctcccagc cacctgctgc atctgttctt gcctgcagcc ctaggatcag 1350
 ggcaaggttt ggcaagaagg aagatctgca ctactttgcy gcctctgctc 1400
 ctccggttcc cccaccccag cttcctgctc aatgctgatc agggacaggt 1450
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ccacctcctg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950
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 caactagaga atggtggtca gtgagacact atagaattac taaggagaag 2250
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 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
1				5					10					15
Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80					85					90
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
				95					100					105
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
				110					115					120
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
				125					130					135
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
				140					145					150
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
				155					160					165
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser

170

175

180

Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser
 185 190 195

Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu
 200 205

<210> 288

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 288

aggcagccac cagctctgtg ctac 24

<210> 289

<211> 27

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-27

<223> Synthetic construct.

<400> 289

cagagaggga agatgaggaa gccagag 27

<210> 290

<211> 42

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-42

<223> Synthetic construct.

<400> 290

ctgtgctact gcccttgac cctggggacc gagtgtctct gc 42

<210> 291

<211> 1570

<212> DNA

<213> Homo sapiens

<400> 291

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tagccgcca gcctcgacgc cgtcccgga cccctgtgct ctgcgcgaag 100

ccctggcccc gggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150

ttcccgcggg gccgtgactg ggcgggcttc agccatgaag accctcatag 200
 cgcctactc cggggtcctg cgcggcgagc gtcaggccga ggctgaccgg 250
 agccagcgct ctacaggagg acctgcgctg tcgcgcgagg ggtctgggag 300
 atggggcact ggatccagca tcctctccgc cctccaggac ctcttctctg 350
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<210> 292
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 292

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Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser	35	40	45	
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn	50	55	60	
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln	65	70	75	
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile	80	85	90	
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu	95	100	105	
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly	110	115	120	
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr	125	130	135	
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu	140	145	150	
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile	155	160	165	
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu	170	175	180	
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu	185	190	195	
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser	200	205	210	
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu	215	220	225	
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly	230	235	240	
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr	245	250	255	
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly				

260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe	Gly Glu Asn Glu Val Tyr	
275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser	Trp Gly Arg Trp Val Gln	
290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe	Ala Pro Cys Ile Phe His	
305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr	Trp Gly Leu Val Pro Tyr	
320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly	Glu Pro Ile Thr Ile Pro	
335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp	Ile Asp Leu Tyr His Thr	
350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu	Phe Asp Lys His Lys Thr	
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Lys Phe Gly Leu Pro Glu Thr Glu Val	Leu Glu Val Asn	
380	385	

<210> 293
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 293
 gctgacctgg ttcccatcta ctcc 24

<210> 294
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 294
 cccacagaca cccatgacac ttcc 24

<210> 295
 <211> 50
 <212> DNA
 <213> Artificial

<220>

<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 295
aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296
<211> 3060
<212> DNA
<213> Homo sapiens

<400> 296
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<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu	1	5	10	15
Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe	20	25	30	
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu	35	40	45	
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln	50	55	60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu	65	70	75	
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala	80	85	90	
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	95	100	105	
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val	110	115	120	
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr	125	130	135	
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu	140	145	150	
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr	155	160	165	

Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe	
				170					175					180	
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys	
				185					190					195	
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	
				200					205					210	
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val	
				215					220					225	
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu	
				230					235					240	
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val	
				245					250					255	
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala	
				260					265					270	
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln	
				275					280					285	
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys	
				290					295					300	
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala	
				305					310					315	
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe	
				320					325					330	
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val	
				335					340					345	
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu	
				350					355					360	
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln								
				365											

<210> 298
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 298
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<210> 299
 <211> 21
 <212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

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<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

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<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

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 acagagtgag actctatgct caaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

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Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly	35	40	45	
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val	50	55	60	
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp	65	70	75	
Gly	Leu	Arg	Pro	Ala	Ser	Ser	Val	Lys	Phe	Leu	Gly	Ser	Ala	Tyr	80	85	90	
Thr	Phe	Phe	Ser	Leu	Thr	Trp	His	Thr	Leu	Leu	Lys	Ala	Ser	Gln	95	100	105	
Gly	Phe	Ser	Leu	Phe	Leu	Gly	Ser	Lys	Tyr	Leu	Glu	Leu	Gln	Glu	110	115	120	
Pro	Ser	Trp	Ser	Gly	Pro	Cys	Pro	Pro	Gly	Gln	Leu	His	Cys	Thr	125	130	135	
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<210> 303
 <211> 1768
 <212> DNA
 <213> Homo sapiens

<400> 303

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<211> 109

<212> PRT

<213> Homo sapiens

<400> 304

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				20					25					30

Asp	Leu	Ser	Leu	Trp	Leu	Trp	Pro	Lys	Pro	Asp	Leu	His	Ser	Gly
				35					40					45

Thr	Arg	Thr	Glu	Val	Ser	Thr	His	Thr	Val	Pro	Ser	Lys	Pro	Gly
				50					55					60

Thr	Ala	Ser	Pro	Cys	Trp	Pro	Leu	Ala	Gly	Ala	Val	Pro	Ser	Pro
				65					70					75

Thr	Val	Ser	Arg	Leu	Glu	Ala	Leu	Thr	Arg	Ala	Val	Gln	Val	Ala
				80					85					90

Glu	Pro	Leu	Gly	Ser	Cys	Gly	Phe	Gln	Gly	Gly	Pro	Cys	Pro	Gly
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<211> 989

<212> DNA

<213> Homo sapiens

<400> 305

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Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln	80	85	90
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys	95	100	105
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu	110	115	120
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val	125	130	135
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala	140	145	150
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu	155	160	165
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp	170	175	180
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr	185	190	195
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val	200	205	210
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly	215	220	225
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg	230	235	240
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly	245	250	255
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<212> PRT

<213> Homo sapiens

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				20					25					30
Gly	Ala	Val	Lys	Pro	Pro	Pro	Asn	Lys	Tyr	Pro	Ile	Phe	Phe	Phe
				35					40					45
Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro
				50					55					60
Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys
				65					70					75
Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala
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Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala
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Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp
				110					115					120
Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala
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Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Lys	Ser	Ser

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<211> 777

<212> PRT

<213> Homo sapiens

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Thr	Glu	Tyr	Gly	Leu	Leu	Ile	Arg	Ser	Leu	Gln	Lys	Lys	Asp	Ser	650	655	660
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<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 315

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Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg		50	55	60
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu		65	70	75
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Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu		125	130	135
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Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu		245	250	255
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly		260	265	270
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu		275	280	285
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Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala				

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 tcagtttgaa tgggcctttg agcaoctctc gccatgtcat ggcccctgtg 1600
 atggctcatg tggatcctga ggagccctgg tccccctgca gtgcccgtt 1650
 catcactgac ttcttggaac atggctatgg gcaactgtctc ttagacaaac 1700
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 acagctgccg ccgcccctgtg ctgccctctg gtgctctggc cacctcaatg 1850
 gccatgccat gtgcagacc aaacactcgc cctggggcga tggcacaccc 1900
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aaggaaa 4407

<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

Met	Ser	Gln	Thr	Gly	Ser	His	Pro	Gly	Arg	Gly	Leu	Ala	Gly	Arg
1				5					10					15

Trp	Leu	Trp	Gly	Ala	Gln	Pro	Cys	Leu	Leu	Leu	Pro	Ile	Val	Pro
			20						25					30

Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu
			35						40				45

Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu
			50						55					60

Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser
			65						70					75

Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu
			80						85					90

Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu
			95						100					105

Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly
			110						115					120

Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp
			125						130					135

Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	140		145		150
Gly Val Leu Gln Tyr Arg Gly Ala Glu Leu His Leu Gln Pro Leu	155		160		165
Glu Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro Gly Ala His Ile	170		175		180
Leu Arg Arg Lys Ser Pro Ala Ser Gly Gln Gly Pro Met Cys Asn	185		190		195
Val Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg Arg Ala	200		205		210
Lys Arg Phe Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val Val	215		220		225
Ala Asp Asp Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg	230		235		240
Tyr Leu Leu Thr Val Met Ala Ala Ala Ala Lys Ala Phe Lys His	245		250		255
Pro Ser Ile Arg Asn Pro Val Ser Leu Val Val Thr Arg Leu Val	260		265		270
Ile Leu Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala	275		280		285
Ala Gln Thr Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn	290		295		300
Thr Pro Glu Asp Ser Gly Pro Asp His Phe Asp Thr Ala Ile Leu	305		310		315
Phe Thr Arg Gln Asp Leu Cys Gly Val Ser Thr Cys Asp Thr Leu	320		325		330
Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ala Arg Ser Cys	335		340		345
Ala Ile Val Glu Asp Asp Gly Leu Gln Ser Ala Phe Thr Ala Ala	350		355		360
His Glu Leu Gly His Val Phe Asn Met Leu His Asp Asn Ser Lys	365		370		375
Pro Cys Ile Ser Leu Asn Gly Pro Leu Ser Thr Ser Arg His Val	380		385		390
Met Ala Pro Val Met Ala His Val Asp Pro Glu Glu Pro Trp Ser	395		400		405
Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu Asp Asn Gly Tyr	410		415		420
Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu His Leu Pro	425		430		435

Val Thr Phe Pro	Gly Lys Asp Tyr Asp	Ala Asp Arg Gln Cys	Gln
	440	445	450
Leu Thr Phe Gly	Pro Asp Ser Arg His	Cys Pro Gln Leu Pro	Pro
	455	460	465
Pro Cys Ala Ala	Leu Trp Cys Ser Gly	His Leu Asn Gly His	Ala
	470	475	480
Met Cys Gln Thr	Lys His Ser Pro Trp	Ala Asp Gly Thr Pro	Cys
	485	490	495
Gly Pro Ala Gln	Ala Cys Met Gly Gly	Arg Cys Leu His Met	Asp
	500	505	510
Gln Leu Gln Asp	Phe Asn Ile Pro Gln	Ala Gly Gly Trp Gly	Pro
	515	520	525
Trp Gly Pro Trp	Gly Asp Cys Ser Arg	Thr Cys Gly Gly Gly	Val
	530	535	540
Gln Phe Ser Ser	Arg Asp Cys Thr Arg	Pro Val Pro Arg Asn	Gly
	545	550	555
Gly Lys Tyr Cys	Glu Gly Arg Arg Thr	Arg Phe Arg Ser Cys	Asn
	560	565	570
Thr Glu Asp Cys	Pro Thr Gly Ser Ala	Leu Thr Phe Arg Glu	Glu
	575	580	585
Gln Cys Ala Ala	Tyr Asn His Arg Thr	Asp Leu Phe Lys Ser	Phe
	590	595	600
Pro Gly Pro Met	Asp Trp Val Pro Arg	Tyr Thr Gly Val Ala	Pro
	605	610	615
Gln Asp Gln Cys	Lys Leu Thr Cys Gln	Ala Arg Ala Leu Gly	Tyr
	620	625	630
Tyr Tyr Val Leu	Glu Pro Arg Val Val	Asp Gly Thr Pro Cys	Ser
	635	640	645
Pro Asp Ser Ser	Ser Val Cys Val Gln	Gly Arg Cys Ile His	Ala
	650	655	660
Gly Cys Asp Arg	Ile Ile Gly Ser Lys	Lys Lys Phe Asp Lys	Cys
	665	670	675
Met Val Cys Gly	Gly Asp Gly Ser Gly	Cys Ser Lys Gln Ser	Gly
	680	685	690
Ser Phe Arg Lys	Phe Arg Tyr Gly Tyr	Asn Asn Val Val Thr	Ile
	695	700	705
Pro Ala Gly Ala	Thr His Ile Leu Val	Arg Gln Gln Gly Asn	Pro
	710	715	720
Gly His Arg Ser	Ile Tyr Leu Ala Leu	Lys Leu Pro Asp Gly	Ser

	725		730		735									
Tyr	Ala	Leu	Asn	Gly	Glu	Tyr	Thr	Leu	Met	Pro	Ser	Pro	Thr	Asp
				740					745					750
Val	Val	Leu	Pro	Gly	Ala	Val	Ser	Leu	Arg	Tyr	Ser	Gly	Ala	Thr
				755					760					765
Ala	Ala	Ser	Glu	Thr	Leu	Ser	Gly	His	Gly	Pro	Leu	Ala	Gln	Pro
				770					775					780
Leu	Thr	Leu	Gln	Val	Leu	Val	Ala	Gly	Asn	Pro	Gln	Asp	Thr	Arg
				785					790					795
Leu	Arg	Tyr	Ser	Phe	Phe	Val	Pro	Arg	Pro	Thr	Pro	Ser	Thr	Pro
				800					805					810
Arg	Pro	Thr	Pro	Gln	Asp	Trp	Leu	His	Arg	Arg	Ala	Gln	Ile	Leu
				815					820					825
Glu	Ile	Leu	Arg	Arg	Arg	Pro	Trp	Ala	Gly	Arg	Lys			
				830					835					

<210> 318

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 318

ccctgaagct gccagatggc tcc 23

<210> 319

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 319

ctgtgctctt cggtgcagcc agtc 24

<210> 320

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 320
ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321
<211> 1197
<212> DNA
<213> Homo sapiens

<400> 321
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gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100
ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150
ttgtggactg gtgtttggta tcttggccct aactctaatt gtcctgtttt 200
gggggagcaa gcacttctgg ccggagggtac ccaaaaaagc ctatgacatg 250
gagcacactt totacagcaa tggagagaag aagaagattt acatggaaat 300
tgatcctgtg accagaactg aaatatccag aagcggaaat ggcactgatg 350
aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400
gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450
attttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500
ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550
aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600
gaccatgtat tggatcaatc cactctaatt atcagtttct gagttacaag 650
actttgagga ggaggagaga gatcttcact ttcctgcca cgaaaaaaaa 700
gggattgaac aaaatgaaca gtgggtggtc cctcaagtga aagtagagaa 750
gaccggtcac gccagacaag caagtgagga agaacttcca ataatgact 800
atactgaaaa tggaatagaa tttgatccca tgctggatga gagaggttat 850
tgttgtatatt actgccgtcg aggcaaccgc tattgccgcc gcgtctgtga 900
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tcatctgtcg tgtcatcatg ccttgtaact ggtgggtggc ccgcatgctg 1000
gggagggtct aataggaggt ttgagctcaa atgcttaaac tgctggcaac 1050
atataataaa tgcattgctat tcaatgaatt tctgcctatg aggcattctg 1100
cccctggtag ccagctctcc agaattactt gtaggtaatt cctctcttca 1150
tgttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaa 1197

<210> 322

<211> 317
 <212> PRT
 <213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu	1	5	10	15
Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	20	25	30	
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	35	40	45	
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	50	55	60	
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	65	70	75	
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	80	85	90	
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	95	100	105	
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	110	115	120	
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	125	130	135	
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	140	145	150	
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	155	160	165	
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	170	175	180	
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	185	190	195	
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	200	205	210	
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	215	220	225	
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	230	235	240	
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	245	250	255	
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	260	265	270	

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
275 280 285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
290 295 300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
305 310 315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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ggcgtgcag cttctgggct tcctgctcag cttcctgggc atggtgggca 150
cgttgatcac caccatcctg ccgcaactggc ggaggacagc gcacgtgggc 200
accaacatcc tcacggccgt gtctacctg aaagggctct ggatggagtg 250
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 ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324
 <211> 239
 <212> PRT
 <213> Homo sapiens

<400> 324

Met	Ala	Ser	Thr	Ala	Val	Gln	Leu	Leu	Gly	Phe	Leu	Leu	Ser	Phe	1	5	10	15
Leu	Gly	Met	Val	Gly	Thr	Leu	Ile	Thr	Thr	Ile	Leu	Pro	His	Trp	20	25	30	
Arg	Arg	Thr	Ala	His	Val	Gly	Thr	Asn	Ile	Leu	Thr	Ala	Val	Ser	35	40	45	
Tyr	Leu	Lys	Gly	Leu	Trp	Met	Glu	Cys	Val	Trp	His	Ser	Thr	Gly	50	55	60	
Ile	Tyr	Gln	Cys	Gln	Ile	Tyr	Arg	Ser	Leu	Leu	Ala	Leu	Pro	Gln	65	70	75	
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Met	Val	Ile	Ser	Cys	Leu	Leu	80	85	90	
Ser	Gly	Ile	Ala	Cys	Ala	Cys	Ala	Val	Ile	Gly	Met	Lys	Cys	Thr	95	100	105	
Arg	Cys	Ala	Lys	Gly	Thr	Pro	Ala	Lys	Thr	Thr	Phe	Ala	Ile	Leu	110	115	120	
Gly	Gly	Thr	Leu	Phe	Ile	Leu	Ala	Gly	Leu	Leu	Cys	Met	Val	Ala	125	130	135	
Val	Ser	Trp	Thr	Thr	Asn	Asp	Val	Val	Gln	Asn	Phe	Tyr	Asn	Pro	140	145	150	
Leu	Leu	Pro	Ser	Gly	Met	Lys	Phe	Glu	Ile	Gly	Gln	Ala	Leu	Tyr	155	160	165	
Leu	Gly	Phe	Ile	Ser	Ser	Ser	Leu	Ser	Leu	Ile	Gly	Gly	Thr	Leu	170	175	180	
Leu	Cys	Leu	Ser	Cys	Gln	Asp	Glu	Ala	Pro	Tyr	Arg	Pro	Tyr	Gln	185	190	195	
Ala	Pro	Pro	Arg	Ala	Thr	Thr	Thr	Thr	Ala	Asn	Thr	Ala	Pro	Ala	200	205	210	
Tyr	Gln	Pro	Pro	Ala	Ala	Tyr	Lys	Asp	Asn	Arg	Ala	Pro	Ser	Val	215	220	225	

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
 230 235

<210> 325
 <211> 2121
 <212> DNA
 <213> Homo sapiens

<400> 325
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 gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac 200
 aaccccgctca cctccgtggt ccagtacgaa gggctctgga ggagctgcgt 250
 gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300
 gacttcacgc catgctgcag gcagtgcgag ccctgatgat cgtaggcatc 350
 gtccctgggtg ccattggcct cctggatatcc atctttgccc tgaaatgcat 400
 ccgcattggc agcatggagg actctgccaa agccaacatg aactgacct 450
 ccgggatcat gttcattgtc tcaggtcttt gtgcaattgc tggagtgtct 500
 gtgtttgccca acatgctggt gactaacttc tggatgtcca cagctaacat 550
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 aagaagatat acgatggagg tgccgcaca gaggacgagg tacaatctta 850
 tccttccaag cagactatg tgtaatgctc taagacctct cagcacgggc 900
 ggaagaaact cccggagagc tcacccaaaa aacaaggaga tcccatctag 950
 atttcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000
 catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050
 ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100
 attttcaatc ctctatttct ttttttaaata ataactttct actctgatga 1150
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 cccctcttc ctcctagtca ataaacccat tgatgatcta tttccagct 1250

tatccccaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300
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 cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400
 cccatgatct cggttttctt aactgtgat cttaaaagt accaaaccaa 1450
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 atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650
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 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750
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 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950
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 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050
 gtctaaaaaa ataaaaata aataatggaa cacagcaagt cctaggaagt 2100
 aggttaaaac taattcttta a 2121

<210> 326
 <211> 261
 <212> PRT
 <213> Homo sapiens

<400> 326
 Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile
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 Leu Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp
 20 25 30
 Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln
 35 40 45
 Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe
 50 55 60
 Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met
 65 70 75
 Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

tgctgcttcc gtgatgtcct tcttggttt catgatggcc atccttggca 400
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 ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500
 ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550
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 atcgcacaa ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750
 tactccagaa gtcagtatgt gtagtttgt atgtttttt aactttacta 800
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<210> 328

<211> 225

<212> PRT

<213> Homo sapiens

<400> 328

Met	Ala	Thr	His	Ala	Leu	Glu	Ile	Ala	Gly	Leu	Phe	Leu	Gly	Gly	1	5	10	15
Val	Gly	Met	Val	Gly	Thr	Val	Ala	Val	Thr	Val	Met	Pro	Gln	Trp	20	25	30	
Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn	35	40	45	
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile	50	55	60	
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro	65	70	75	
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met	80	85	90	
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr	95	100	105	
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu	110	115	120	
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile	125	130	135	
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	140	145	150	
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu	155	160	165	
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala	170	175	180	
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr	185	190	195	
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His	200	205	210	

Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
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<210> 329
 <211> 1315
 <212> DNA
 <213> Homo sapiens

<400> 329

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cagctatgta gacccccgcc cccacctcca aactgcacc cttctgccct 1250

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tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met Ala Ser Ala Gly Met Gln Ile Leu Gly Val Val Leu Thr Leu
1 5 10 15

Leu Gly Trp Val Asn Gly Leu Val Ser Cys Ala Leu Pro Met Trp
20 25 30

Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val
35 40 45

Val Trp Glu Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly
50 55 60

Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln
65 70 75

Asp Leu Gln Ala Ala Arg Ala Leu Cys Val Ile Ala Leu Leu Val
80 85 90

Ala Leu Phe Gly Leu Leu Val Tyr Leu Ala Gly Ala Lys Cys Thr
95 100 105

Thr Cys Val Glu Glu Lys Asp Ser Lys Ala Arg Leu Val Leu Thr
110 115 120

Ser Gly Ile Val Phe Val Ile Ser Gly Val Leu Thr Leu Ile Pro
125 130 135

Val Cys Trp Thr Ala His Ala Ile Ile Arg Asp Phe Tyr Asn Pro
140 145 150

Leu Val Ala Glu Ala Gln Lys Arg Glu Leu Gly Ala Ser Leu Tyr
155 160 165

Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu Gly Gly Gly Leu
170 175 180

Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly Pro Ser His
185 190 195

Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser Arg Gly
200 205 210

Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val
215 220

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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gttccttggc atggtgggga ctcttgccac aacccttctg cctcagtggc 200
ggagtatcag cttttgttgg cagcaacatt attgtctttg agaggctctg 250
ggaagggctc tggatgaatt gcatccgaca agccagggtc cggttgcaat 300
gcaagttcta tagctccttg ttggctctcc cgctgccct ggaaacagcc 350
cgggccctca tgtgtgtggc tgttgctctc tccttgatcg ccctgcttat 400
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cacttttctt tggctgggca agcgtgctg tcctcttcat tggagggggg 650
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ccaagtatgg actatggta atgtttttta taaagtctg ctagaaactg 850
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acattctgac ttcagggtga ttaaatgcat tgactattgt tggacccaat 1000
cgctgctcca attttcatat tctaaattca agtataccca taatcattag 1050
caagtgtaca atgatggact acttattact ttttgacct catgtattat 1100
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<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

1	5	10	15
Tyr Ser Ser Leu Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg	20	25	30
Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu	35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn	50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe	65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala	80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly	95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser	110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys	125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly	140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu	155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val	170		

<210> 333

<211> 535

<212> DNA

<213> Homo sapiens

<400> 333

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ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150
agaagtatcc agtgggtggcc atcccctgcc ccatcacata cctaccagtt 200
tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250
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tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400
ggtagggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

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ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500

tttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

Met Lys Ile Thr Gly Gly Leu Leu Leu Cys Thr Val Val Tyr
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Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
20 25 30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
35 40 45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
50 55 60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
65 70 75

Arg Val Gln Phe Leu His Asp Gly Ser Cys
80 85

<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

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tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccaggt 150

ggcataagtg gaaataaact caagctgatg cttcaaaaac gagaagcacc 200

tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250

tccttggcag cctgaagcgc cagaagcggc agctgtggga cgggactcgg 300

cccgaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350

agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450

gcaattggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500

ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaat 550

agcgattctc ttcattgtatc tcctaattgcc ttacactact tggttttctga 600

tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
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<210> 336
<211> 148
<212> PRT
<213> Homo sapiens

<400> 336
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1 5 10 15
Leu Ala Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
20 25 30
Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
35 40 45
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
50 55 60
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
65 70 75
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
80 85 90
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
95 100 105
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
110 115 120
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
125 130 135
Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
140 145

<210> 337
<211> 1310
<212> DNA
<213> Homo sapiens

<400> 337
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tgaaggggtg ggtgatgagg tgaccgtcct tttctcgggtg cttgcctgcc 150
ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200
gaccactgc ccagccgctc agggacccca acgcatccc agcccagcgc 250

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 aaaaaaaaa 1310

<210> 338
 <211> 246
 <212> PRT
 <213> Homo sapiens

<400> 338
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 20 25 30
 Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly
 35 40 45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	
				50					55					60	
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	
				65					70					75	
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	
				80					85					90	
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	
				95					100					105	
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	
				110					115					120	
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	
				125					130					135	
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	
				140					145					150	
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	
				155					160					165	
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	
				170					175					180	
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	
				185					190					195	
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
				200					205					210	
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	
				215					220					225	
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	
				230					235					240	
Phe	Ala	Met	Tyr	Arg	Pro										
				245											

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

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tcaggccagc ctcatcagtc gctgtgactt ggcccaggtg ctgcagctgg 250

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<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met	Thr	Lys	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Ser	Phe	Leu	Ala
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Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val
				20					25					30

Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser
			35						40					45

Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser
			50						55					60

Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe
			65						70					75

Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser
			80						85					90

Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn
			95						100					105

Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala
			110						115					120

Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly
			125						130					135

Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg

<210> 341
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 341
 ccctccaagg atgacaaagg cgc 23

<210> 342
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-29
 <223> Synthetic construct.

<400> 342
 ggtcagcagc tttcttgccc taaatcagg 29

<210> 343
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 343
 atctcaggcg gcatcctgtc agcc 24

<210> 344
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 344
 gtggatgcct gcaagaaggt tggg 24

<210> 345
 <211> 45
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 345
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<210> 346
<211> 2575
<212> DNA
<213> Homo sapiens

<400> 346
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<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

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1 5 10 15

Phe Leu Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val
20 25 30

Ala Met Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr
35 40 45

Ala Gln Ala Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp
50 55 60

Phe Gly Glu Ser Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly
65 70 75

Glu Glu Tyr Ser Pro Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu
80 85 90

Arg Glu Asp Gln Leu Leu Val Ala Val Ala Leu Pro Gln Ala Arg
95 100 105

Arg Asn Gln Ser Gln Gly Arg Arg Gly Gly Ser Tyr Arg Leu Ile
110 115 120

Lys Gln Pro Arg Arg Gln Asp Lys Glu Ala Pro Lys Arg Asp Trp
125 130 135

Gly Ala Asp Glu Asp Gly Glu Val Ser Glu Glu Glu Glu Leu Thr
140 145 150

Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln Glu Ala Leu Ser Ala
155 160 165

Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val Arg His Pro Leu
170 175 180

Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr Ala Ser Val
185 190 195

Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu Arg Thr
200 205 210

Val His Ser Ile Leu Asp Thr Val Pro Arg Ala Phe Leu Lys Glu
215 220 225

Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser
230 235 240

Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Lys Leu Leu
245 250 255

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly	260	265	270
Ala Thr Arg Ala	Thr Gly Asp Val Leu Val	Phe Met Asp Ala His	275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe			

545	550	555
Gly Ser Pro Gln His Leu Cys Phe Ala Val Arg Gln Glu Gln Val		
560	565	570
Ile Leu Gln Asn Cys Thr Glu Glu Gly Leu Ala Ile His Gln Gln		
575	580	585
His Trp Asp Phe Gln Glu Asn Gly Met Ile Val His Ile Leu Ser		
590	595	600
Gly Lys Cys Met Glu Ala Val Val Gln Glu Asn Asn Lys Asp Leu		
605	610	615
Tyr Leu Arg Pro Cys Asp Gly Lys Ala Arg Gln Gln Trp Arg Phe		
620	625	630
Asp Gln Ile Asn Ala Val Asp Glu Arg		
635		

<210> 348

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 348

ggagaggtgg tggccatgga cag 23

<210> 349

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 349

ctgtcactgc aaggagccaa cacc 24

<210> 350

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 350

tatgtcgctg cgagggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351
 <211> 2524
 <212> DNA
 <213> Homo sapiens

<400> 351
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 tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150
 tcttcatact cccctcgaac cccaccagcc ccagcccgcc ccccgctgtg 200
 caggggaggg ccctcggccc cacgtcatgt gtgcgtgtgg gagcgagcac 250
 ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtcctg 300
 cctggcactg cccccccagc cccccatca ggctttgagg aggggccgcc 350
 ctcatcccaa taccctggg ctatcgtgtg gggcccacc gtgtctcgag 400
 aggatggagg ggaccccaac tctgccaatc ccgatttct ggactatggg 450
 tttgcagccc ctcatgggct cgcaacccca ccccact cagactccat 500
 gcgaggtgat ggagatgggc ttatccttgg agaggcacct gccaccctgc 550
 ggccattcct gttcgggggc cgtggggaag gtgtggaccc ccagctctat 600
 gtcacaatta ccattctcat catcattgtt ctctgtggcca ctggcatcat 650
 cttcaagttc tgctgggacc gcagccagaa gcgacgcaga ccctcagggc 700
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 caccctgac catgaggagc cccgaggggg accccggcct gggatgcccc 850
 accccaaggg ggctccagcc ttccagttga accggtgagg gcaggggcaa 900
 tgggatggga gggcaaagag ggaaggcaac ttaggtcttc agagctgggg 950
 tgggggtgcc ctctggatgg gtagtgagga ggcaggcgtg gcctcccaca 1000
 gccctggcc ctccaaggg ggctggacca gctcctctct gggaggcacc 1050
 cttccttctc ccagtctctc aggatctgtg tctattctc tgctgcccat 1100
 aactccaact ctgccctctt tggtttttct tcatgccacc ttgtctaaga 1150
 caactctgcc ctcttaacct tgattcccc tctttgtctt gaacttcccc 1200
 ttctattctg gcctaccctt tggttcctga ctgtgccctt tccctcttcc 1250
 tctcaggatt cccctggtga atctgtgatg cccccaatgt tgggggtgcag 1300

Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
 20 25 30
 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
 35 40 45
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
 50 55 60
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
 65 70 75
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
 80 85 90
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
 95 100 105
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
 110 115 120
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
 125 130 135
 Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
 140 145 150
 Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
 155 160 165
 Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
 170 175 180
 Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
 185 190 195
 Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
 200 205 210
 Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
 215 220 225
 Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
 230 235 240
 Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

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tccgggggttc tggcccctgc ggtgctcaca gacgatgttc cacaggagcc 150
 cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggccccca 250
 gccccaccg tcgcgccagg acccgaggac agcacgcgcg aggagcggct 300
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 ctgagaaagt tttctgcctc ctgaagcgaa taaagggggc gcgcccggcc 450
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354

<211> 121

<212> PRT

<213> Homo sapiens

<400> 354

Met	Ala	Ser	Cys	Leu	Ala	Leu	Arg	Met	Ala	Leu	Leu	Leu	Val	Ser
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Gly	Val	Leu	Ala	Pro	Ala	Val	Leu	Thr	Asp	Asp	Val	Pro	Gln	Glu
				20					25					30
Pro	Val	Pro	Thr	Leu	Trp	Asn	Glu	Pro	Ala	Glu	Leu	Pro	Ser	Gly
				35					40					45
Glu	Gly	Pro	Val	Glu	Ser	Thr	Ser	Pro	Gly	Arg	Glu	Pro	Val	Asp
				50					55					60
Thr	Gly	Pro	Pro	Ala	Pro	Thr	Val	Ala	Pro	Gly	Pro	Glu	Asp	Ser
				65					70					75
Thr	Ala	Gln	Glu	Arg	Leu	Asp	Gln	Gly	Gly	Gly	Ser	Leu	Gly	Pro
				80					85					90
Gly	Ala	Ile	Ala	Ala	Ile	Val	Ile	Ala	Ala	Leu	Leu	Ala	Thr	Cys
				95					100					105
Val	Val	Leu	Ala	Leu	Val	Val	Val	Ala	Leu	Arg	Lys	Phe	Ser	Ala
				110					115					120

Ser

<210> 355

<211> 2134

<212> DNA

<213> Homo sapiens

<400> 355

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 gttggccggc ggcgggccgg gacgggcatg gccctgctgc tgtgcctggt 100

gtgcctgacg gcggcgctgg cccacggctg tctgcactgc cacagcaact 150
 tctccaagaa gttctccttc taccgccacc atgtgaactt caagtcctgg 200
 tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250
 cgacacgatg aaggagctgc acctggccat ccccgccaag atcaccggg 300
 agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350
 taccagggga agatgtactt ccccggtat ttccccaacg agctgcgaaa 400
 catcttccgg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450
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 cgaccccgga cagagctgag ctggccaggg ccaggagggc gggagggagg 2050
 gaatgggggt gggctgtgcg cagcatcagc gcctgggcag gtccgcagag 2100
 ctgcgggatg tgattaaagt ccctgatgtt tctc 2134

<210> 356

<211> 157

<212> PRT

<213> Homo sapiens

<400> 356

Met	Ala	Leu	Leu	Leu	Cys	Leu	Val	Cys	Leu	Thr	Ala	Ala	Leu	Ala	1	5	10	15
His	Gly	Cys	Leu	His	Cys	His	Ser	Asn	Phe	Ser	Lys	Lys	Phe	Ser	20	25	30	
Phe	Tyr	Arg	His	His	Val	Asn	Phe	Lys	Ser	Trp	Trp	Val	Gly	Asp	35	40	45	
Ile	Pro	Val	Ser	Gly	Ala	Leu	Leu	Thr	Asp	Trp	Ser	Asp	Asp	Thr	50	55	60	
Met	Lys	Glu	Leu	His	Leu	Ala	Ile	Pro	Ala	Lys	Ile	Thr	Arg	Glu	65	70	75	
Lys	Leu	Asp	Gln	Val	Ala	Thr	Ala	Val	Tyr	Gln	Met	Met	Asp	Gln	80	85	90	
Leu	Tyr	Gln	Gly	Lys	Met	Tyr	Phe	Pro	Gly	Tyr	Phe	Pro	Asn	Glu	95	100	105	
Leu	Arg	Asn	Ile	Phe	Arg	Glu	Gln	Val	His	Leu	Ile	Gln	Asn	Ala	110	115	120	
Ile	Ile	Glu	Arg	His	Leu	Ala	Pro	Gly	Ser	Trp	Gly	Gly	Gly	Gln	125	130	135	
Leu	Ser	Arg	Glu	Gly	Pro	Ser	Leu	Ala	Pro	Glu	Gly	Ser	Met	Pro				

140

145

150

Ser Pro Arg Gly Asp Leu Pro
155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

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ttgagaaatc ctcatggtt cctggtgctg cccaggaacc cacgtggctc 150
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200
cataggcttc ttccaggatt tagaaatacc agcagtgcc atactccata 250
gcatggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300
gaggttctga cactacaaa catcactggg aacaccatct gcctctttcg 350
cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400
ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450
gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500
tcagattcat ctctcctga taatgaacaa ggcctcccca gagtatgaag 550
agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600
ctcttttattc tgggtggacag tggtagaaa gaaaatggga aggtgatatc 650
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catgtgcaaa acttttgtga tggattccta agtggaaaat tgttgaaaga 800
aaatcgtgaa tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850
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aactcaaato tcagagacac taaacaacag gatcactagg cctgccaacc 950
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tctcttcttc cttcttttaa atttcatatc ctactccct atccaatttc 1100
cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150
tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200

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cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300
gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350
tcaaaaacca aaggatggtt ttaaacacct ttgtgaaatt gtctttttgc 1400
cagaagttaa aggctgtctc caagtccttg aactcagcag aaatagacca 1450
tgtgaaaact ccatgcttgg ttagcatctc caactcccta tgtaaataca 1500
caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu	1	5	10	15
Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser	20	25	30	
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp	35	40	45	
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val	50	55	60	
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu	65	70	75	
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser	80	85	90	
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr	95	100	105	
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu	110	115	120	
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe	125	130	135	
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val	140	145	150	
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu	155	160	165	
Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His	170	175	180	
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe	185	190	195	

Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 359
 ccagcagtgc ccatactcca tagc 24

<210> 360
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 360
 tgacgagtgg gatacactgc 20

<210> 361
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 361
 gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 362
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50
ccggcgcggg tggcggagag atcagaagcc tcttcccca ggcgagccaa 100
cctcagcggg gacccgggct cagggacgcg gcgcggcgg cggcgactgc 150
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200
cccagacagc cggcgctggc tgtggtcgtt gctggcgggc gcgcttgggc 250
tcttgacagc tggagtatca gccttggaag tatatacgcc aaaagaaatc 300
ttcgtggcaa atggtacaca aggaagctg acctgcaagt tcaagtctac 350
tagtacgact ggcgggttga cctcagtctc ctggagcttc cagccagagg 400
gggccgacac tactgtgtcg tttttccact actccaagg gcaagtgtac 450
cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag ttatacaca 550
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600
cctggacaca ttaggctcta tgcgtagaa aaagagaatt tgcctgtgtt 650
tccagtttgg gtagtggtgg gcatagttac tgctgtggtc ctaggtctca 700
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800
gcaggctcct cggaagtccc cctccgacac tgagggctct gtaaagagtc 850
tgctttctgg atctcaccag ggcccagtca tatatgcaca gttagaccac 900
tccggcggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950
tgoggatatc cgaaagaatt aagagaatac ctagaacata tcctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050
 atgtagcctt ggagaccag gcaaggacaa gtacacgtgt actcacagag 1100
 ggagagaaaag atgtgtacaa aggatatgta taaatattct atttagtcat 1150
 cctgatatga ggagccagtg ttgcatgatg aaaagatggt atgattctac 1200
 atatgtaccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250
 caattgggag atttcagaaa cattcctttc accatcattt agaaatgggt 1300
 tgccttaatg gagacaatag cagatcctgt agtatttcca gtagacatgg 1350
 ccttttaatc taagggctta agactgatta gtcttagcat ttactgtagt 1400
 tggaggatgg agatgctatg atggaagcat acccaggggtg gccttttagca 1450
 cagtatcagt accattttatt tgtctgccgc ttttaaaaaa taccattgg 1500
 ctatgccact tgaaaacaat ttgagaagtt tttttgaagt ttttctcact 1550
 aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600
 tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650
 attagcaaag gataaatgcc gaaggtcact tcattctgga cacagttgga 1700
 tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750
 cgtggagagt aaaaagtatc ggtttta 1777

<210> 364
 <211> 269
 <212> PRT
 <213> Homo sapiens

<400> 364
 Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp
 1 5 10 15
 Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu
 20 25 30
 Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu
 35 40 45
 Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe
 50 55 60
 Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser
 65 70 75
 Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr
 80 85 90
 Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp
 95 100 105

Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile	110	115	120
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys	125	130	135
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile	140	145	150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val	155	160	165
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr	170	175	180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn	185	190	195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser	200	205	210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly	215	220	225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile	230	235	240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile	245	250	255
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn		260	265	

<210> 365
 <211> 1321
 <212> DNA
 <213> Homo sapiens

<400> 365
 gcgggctgtg cagagacgcc atgtaccggc tcctgtcagc agtgactgcc 50
 cgggctgccg cccccggggg cttggcctca agctgcggac gacgcggggg 100
 ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcggggggc 150
 tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
 aggggcgcgg ccccggcgca gtccccgcg gcccccgacc ctgaggcgctc 250
 gcctctggcc gagccgccac aggagcagtc cctcgccccg tggctctccgc 300
 agaccccggc gccgccctgc tccagggtgt tcgccagagc catcgagagc 350
 agccgcgacc tgctgcacag gatcaaggat gaggtggggc caccgggcat 400
 agtggttgga gtttctgtag atggaaaaga agtctggtca gaaggtttag 450
 gttatgctga tggtgagaac cgtgtaccat gtaaaccaga gacagttatg 500

cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggtttc tgtcacaaca 650
 agattactga tttcccatTT aagtggaatt cgtcattatg aaaaggacat 700
 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
 agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
 gattttacta aattttaaac agagcaggag aatgaagcca aatgccggaa 850
 ttcaaaacct ggcaagaaaa agaatgattt tgaacaaggc gaattatatt 900
 tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaaat 950
 gatcccttTgt tcttcaaacc tggtagtcag tttttgtatt caacttttgg 1000
 ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaattatt 1050
 tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100
 caggaagaaa acgagccagt gatttacaat agagcaaggT aatgaatac 1150
 cttctgctgt gtctagctat atcgcatctt aacactattt tattaattaa 1200
 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacattttgg 1250
 gagcttttct acatgtctgt tttctcatct gtaaagtgaa ggaagtaaaa 1300
 catgtttata aagtaaaaaa a 1321

<210> 366
 <211> 373
 <212> PRT
 <213> Homo sapiens

<400> 366
 Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro
 1 5 10 15
 Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg
 20 25 30
 Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly
 35 40 45
 Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu
 50 55 60
 Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu
 65 70 75
 Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro
 80 85 90

Trp	Ser	Pro	Gln	Thr	Pro	Ala	Pro	Pro	Cys	Ser	Arg	Cys	Phe	Ala	
				95					100					105	
Arg	Ala	Ile	Glu	Ser	Ser	Arg	Asp	Leu	Leu	His	Arg	Ile	Lys	Asp	
				110					115					120	
Glu	Val	Gly	Ala	Pro	Gly	Ile	Val	Val	Gly	Val	Ser	Val	Asp	Gly	
				125					130					135	
Lys	Glu	Val	Trp	Ser	Glu	Gly	Leu	Gly	Tyr	Ala	Asp	Val	Glu	Asn	
				140					145					150	
Arg	Val	Pro	Cys	Lys	Pro	Glu	Thr	Val	Met	Arg	Ile	Ala	Ser	Ile	
				155					160					165	
Ser	Lys	Ser	Leu	Thr	Met	Val	Ala	Leu	Ala	Lys	Leu	Trp	Glu	Ala	
				170					175					180	
Gly	Lys	Leu	Asp	Leu	Asp	Ile	Pro	Val	Gln	His	Tyr	Val	Pro	Glu	
				185					190					195	
Phe	Pro	Glu	Lys	Glu	Tyr	Glu	Gly	Glu	Lys	Val	Ser	Val	Thr	Thr	
				200					205					210	
Arg	Leu	Leu	Ile	Ser	His	Leu	Ser	Gly	Ile	Arg	His	Tyr	Glu	Lys	
				215					220					225	
Asp	Ile	Lys	Lys	Val	Lys	Glu	Glu	Lys	Ala	Tyr	Lys	Ala	Leu	Lys	
				230					235					240	
Met	Met	Lys	Glu	Asn	Val	Ala	Phe	Glu	Gln	Glu	Lys	Glu	Gly	Lys	
				245					250					255	
Ser	Asn	Glu	Lys	Asn	Asp	Phe	Thr	Lys	Phe	Lys	Thr	Glu	Gln	Glu	
				260					265					270	
Asn	Glu	Ala	Lys	Cys	Arg	Asn	Ser	Lys	Pro	Gly	Lys	Lys	Lys	Asn	
				275					280					285	
Asp	Phe	Glu	Gln	Gly	Glu	Leu	Tyr	Leu	Arg	Glu	Lys	Phe	Glu	Asn	
				290					295					300	
Ser	Ile	Glu	Ser	Leu	Arg	Leu	Phe	Lys	Asn	Asp	Pro	Leu	Phe	Phe	
				305					310					315	
Lys	Pro	Gly	Ser	Gln	Phe	Leu	Tyr	Ser	Thr	Phe	Gly	Tyr	Thr	Leu	
				320					325					330	
Leu	Ala	Ala	Ile	Val	Glu	Arg	Ala	Ser	Gly	Cys	Lys	Tyr	Leu	Asp	
				335					340					345	
Tyr	Met	Gln	Lys	Ile	Phe	His	Asp	Leu	Asp	Met	Leu	Thr	Thr	Val	
				350					355					360	
Gln	Glu	Glu	Asn	Glu	Pro	Val	Ile	Tyr	Asn	Arg	Ala	Arg			
				365					370						

<210> 367

<211> 30
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-30
<223> Synthetic construct.

<400> 367
tggaagagaa gtctgggtcag aaggttttagg 30

<210> 368
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 368
catttggtt cattctcctg ctctg 25

<210> 369
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 369
aaaacctcag aacaactcat ttgacacc 28

<210> 370
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 370
gtctcaccat gggtgctctt gccaaattgt gggaagcagg g 41

<210> 371
<211> 1150
<212> DNA
<213> Homo sapiens

<400> 371
gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggg gggaagaagc cgagatggcg gcagccagcg 100
 ctggggcaac ccggctgctc ctgctcttgc tgatggcggg agcagcgccc 150
 agtcgagccc ggggcagcgg ctgccgggcc gggactgggt gcgagggggc 200
 tggggcggaa ggtcgagagg gcgaggcctg tggcacgggt gggctgctgc 250
 tggagcactc atttgagatc gatgacagtg ccaacttccg gaagcggggc 300
 tcactgctct ggaaccagca ggatggtacc ttgtccctgt cacagcggca 350
 gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400
 gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450
 gaagctgggt gctatgtctc ctcccttgtc cctgcgtgct ccctggtgga 500
 gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550
 tgggtggcgt gtcggtgggt acgcaccccg ggggctgccg gggccatgag 600
 gtggaggacg tggacctgga gctgttcaac acctcgggtg agctgcagcc 650
 gcccaccaca gccccaggcc ctgagacggc ggccttcatt gagcgcctgg 700
 agatggaaca ggcccagaag gccagaacc ccaggagca gaagtccttc 750
 ttgcgcaaat actggatgta catcattccc gtcgtcctgt tcctcatgat 800
 gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850
 gtggtggggg tagtggcctt tgctgtgtgc caccctccct gtaagtctat 900
 ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950
 agcttccagc agccaaaagc aactgttgtt ttggcaagac ggtcctgatg 1000
 tacaagcttg attgaaattc actgctcact tgatacgtta ttcagaaaacc 1050
 caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100
 ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10					15

Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
			20						25					30

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
			35						40					45

Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	
				50					55					60	
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	
				65					70					75	
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	
				80					85					90	
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	
				95					100					105	
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	
				110					115					120	
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	
				125					130					135	
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	
				140					145					150	
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	
				155					160					165	
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	
				170					175					180	
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	
				185					190					195	
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	
				200					205					210	
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	
				215					220					225	
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	
				230					235					240	
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
				245					250					255	
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		
				260					265						

<210> 373
 <211> 1706
 <212> DNA
 <213> Homo sapiens

<400> 373
 ggagcgctgc tggaaccgca gccggagccg gagccacagc ggggaggggtg 50
 gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100
 cagcaggtcg tccgggggcc caccatgctg gtgactgcct accttgcttt 150
 tgtaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200

ctaaaccctt tggaagggcc tgcagcaatc cctccttcct tcggtttcaa 250
 ctggacttct atcagggtcta cttcctggcc ctggcagctg attggcttca 300
 ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggctc 350
 aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400
 ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450
 cctcttctcc ctgaactact caatatgtgt ctttaacaaa ctctctcaag 500
 actactttgt gctgctagtgt gggcgagcac ttggtgggct gtccacagcc 550
 ctgctcttct cagccttcga ggcttggtat atccatgagc acgtggaacg 600
 gcatgacttc cctgctgagt ggatcccagc tacctttgct cgagctgcct 650
 tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700
 gccagctgga tagggctggg gcctgtagcg ccctttgtgg ctgccatccc 750
 tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800
 atgaccggca gcgtgccttc tcaaggacct gtgctggagg cctgcgctgc 850
 ctctgtcgg accgcgcgt gctgctgctg ggcaccatac aagctctatt 900
 tgagagtgtc atcttcatct ttgtcttcct ctggacacct gtgctggacc 950
 cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000
 ctgcttggct cttccctgta ccgtatcgcc acctccaaga ggtaccacct 1050
 tcagcccatg cacctgctgt cccttgcctg gctcatcgtc gtcttctctc 1100
 tcttcatgtt gactttctct accagcccag gccaggagag tccgggtggag 1150
 tccttcatag cctttctact tattgagttg gcttgtggat tatactttcc 1200
 cagcatgagc ttcctacgga gaaaggatgat ccctgagaca gagcaggctg 1250
 gtgtactcaa ctggttcggg gtacctctgc actcaactggc ttgcctaggg 1300
 ctcttctgct tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350
 cagcatttgc tctgctgtca tggatgatgc tctgctggca gtggtgggac 1400
 tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450
 gaggagccct atgccctga gctgtaaccc cactccagga caagatagct 1500
 gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550
 gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600
 gggaggacat gatgggggtg atggactgga aagaaggctg caaaagttcc 1650

ctctgtgtta ctcccatitta gaaaataaac actttttaaat gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser
1 5 10 15

Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly
20 25 30

Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe
35 40 45

Tyr Gln Val Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala
50 55 60

Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly
65 70 75

Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu
80 85 90

Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys
95 100 105

Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu
110 115 120

Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala
125 130 135

Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala
140 145 150

Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu
155 160 165

Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val
170 175 180

Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp
185 190 195

Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu
200 205 210

Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu Asn
215 220 225

Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu
230 235 240

Arg Cys Leu Leu Ser Asp Arg Arg Val	Leu Leu Leu Gly Thr Ile
245	250 255
Gln Ala Leu Phe Glu Ser Val Ile Phe	Ile Phe Val Phe Leu Trp
260	265 270
Thr Pro Val Leu Asp Pro His Gly Ala	Pro Leu Gly Ile Ile Phe
275	280 285
Ser Ser Phe Met Ala Ala Ser Leu Leu	Gly Ser Ser Leu Tyr Arg
290	295 300
Ile Ala Thr Ser Lys Arg Tyr His Leu	Gln Pro Met His Leu Leu
305	310 315
Ser Leu Ala Val Leu Ile Val Val Phe	Ser Leu Phe Met Leu Thr
320	325 330
Phe Ser Thr Ser Pro Gly Gln Glu Ser	Pro Val Glu Ser Phe Ile
335	340 345
Ala Phe Leu Leu Ile Glu Leu Ala Cys	Gly Leu Tyr Phe Pro Ser
350	355 360
Met Ser Phe Leu Arg Arg Lys Val Ile	Pro Glu Thr Glu Gln Ala
365	370 375
Gly Val Leu Asn Trp Phe Arg Val Pro	Leu His Ser Leu Ala Cys
380	385 390
Leu Gly Leu Leu Val Leu His Asp Ser	Asp Arg Lys Thr Gly Thr
395	400 405
Arg Asn Met Phe Ser Ile Cys Ser Ala	Val Met Val Met Ala Leu
410	415 420
Leu Ala Val Val Gly Leu Phe Thr Val	Val Arg His Asp Ala Glu
425	430 435
Leu Arg Val Pro Ser Pro Thr Glu Glu	Pro Tyr Ala Pro Glu Leu
440	445 450

<210> 375

<211> 1098

<212> DNA

<213> Artificial

<400> 375

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gctccccgcg tgcgtcgcg cccacggctt ccgtatccat gattatttgt 150
actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200
cctgccaaagg actttggtgg tatctttcac acaaggtatg agcagattca 250

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ccttgtcccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300
 tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350
 ctctccaaga ctcggtggtt ccaggagcac ggcgggcggg cggatgatcat 400
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
 acagtaccca gcgcacagct gacatccccg cctcttctct gctcggccga 500
 gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550
 catcatttcc atcccagtc atgtcaccag catccccacc tttgagctgc 600
 tgcaaccgcc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650
 ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
 aatttgaga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750
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 cccagggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850
 cccagggct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900
 gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
 taccagggt ctctgcacag tgaccttcac agcagttgtt ggagtgggtt 1000
 aaagagctgg tgtttgggga ctcaataaac cctcactgac ttttagcaa 1050
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu
 1 5 10 15

Pro Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu
 20 25 30

Tyr Phe Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr
 35 40 45

Ala Thr Pro Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr
 50 55 60

Glu Gln Ile His Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly
 65 70 75

Glu Leu Ser Asn Gly Phe Phe Ile Gln Asp Gln Ile Ala Leu Val
 80 85 90

Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln
 95 100 105
 Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp
 110 115 120
 Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg
 125 130 135
 Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr
 140 145 150
 Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile
 155 160 165
 Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu
 170 175 180
 Leu Gln Pro Pro Trp Thr Phe Trp
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<210> 377
 <211> 496
 <212> DNA
 <213> Artificial

<220>
 <221> unsure
 <222> 396
 <223> unknown base

<400> 377
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 ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctctccta 150
 ctggccctac ggctgtcact gcggactagg tggcagaggc caaccctaaag 200
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250
 aagaccagc ggtgcggcat ctacaaggac aacaacaaaa gcagcatata 300
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5					10					15
Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
			20					25						30
Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
			35						40					45
Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
			50						55					60
Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
			65						70					75
Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
			80						85					90
His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
			95						100					105
Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu				
				110					115					

<210> 379

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 379

ctgcctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 380

cagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 381

ctgaacaaga tggtaagca agtgactggg aaaatgccca tcttc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

ctcgcttctt ccttctggat gggggcccag gggggccagg agagtataaa 50

ggcgatgtgg aggggtgccc gcacaaccag acgcccagtc acaggcgaga 100

gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150

ctcctggggg gcccacactg ggcagggaag atgtatggcc ctggaggagg 200

caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250

gggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttgga 300

gactcctggg acgtgaaact gggagcotta ggtgggaata cccaggaagt 350

caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400

ctttcctccg gggatggtc atgtacacca gcaaggaccg ctatttctat 450

tttgggaagc ttgatggcca gatctctctt gcctacccca gccaaaggagg 500

gcagggtgctg gtgggcatct atggccagta tcaactcctt ggcatacaaga 550

gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600

ccagttaatc tcacatactc agcaaactca cccgtgggtc gctaggggtg 650

ggtatggggc catccgagct gaggccatct gtgtgggtgt ggctgatggt 700

actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750

gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met His Arg Pro Glu Ala Met Leu Leu Leu Thr Leu Ala Leu
1 5 10 15

Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly
20 25 30

Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr
35 40 45

Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln
 50 55 60
 Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly
 65 70 75
 Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr
 80 85 90
 Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met
 95 100 105
 Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly
 110 115 120
 Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val
 125 130 135
 Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly
 140 145 150
 Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro
 155 160 165
 Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg
 170 175

<210> 384
 <211> 2379
 <212> DNA
 <213> Homo sapiens

<400> 384
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 atacagatgt ggcagctcag gtagcccca attgcctgga agaatacatc 150
 atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200
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 tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350
 atgttcacaa atcgggtccat ctccaagggt gtccaatttt tcttcctggg 400
 tgtcagcgag ccctgactca ctacagtgc gctgacagg gctgtcatgc 450
 aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500
 acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag 550
 cactggttat agccccact gtcttactga caatgctttc ttctgccgaa 600
 cgaggatgcc ctaagggtg taggtgtgaa ggcaaatgg tatattgtga 650

atctcagaaa ttacaggaga taccctcaag tatatctgct ggttgcttag 700
 gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt 750
 aaagggctca accagctcac ctggctatac cttgaccata accatatcag 800
 caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850
 ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900
 gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950
 gggatctgaa cagtttcggg gcttgcgga gctgctgagt ttacatttac 1000
 ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc 1050
 aacctggaac ttttgacct gggatataac cggatccgaa gtttagccag 1100
 gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150
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 tcgaagcttt cagtggacct agtgttttcc agtgtgtccc gaatctgcag 1350
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 aatgcagcag aaatatttgc tcccttgtaa actggctgaa aagttttaaa 1500
 ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550
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 ctgctcatcc tgctggttat ctacgtgtca tggaagcggg acctgcgag 1850
 catgaagcag ctgcagcagc gctccctcat gcgaaggcac aggaaaaaga 1900
 aaagacagtc cctaaagcaa atgactccca gcaccagga attttatgta 1950
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 gggacctgc acctataaca aatcgggctc cagggagtgt gaggtatgaa 2050
 ccattgtgat aaaaagagct cttaaaagct gggaaataag tgggtgcttta 2100

ttgaactctg gtgactatca agggaacgcg atgccccccc tcccccttccc 2150
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 tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt 2250
 aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300
 ttgtataaga ccctttactg attccattaa tgtcgcattt gttttaagat 2350
 aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385
 <211> 513
 <212> PRT
 <213> Homo sapiens

<400> 385

Met	Gly	Phe	Asn	Val	Ile	Arg	Leu	Leu	Ser	Gly	Ser	Ala	Val	Ala	1	5	10	15
Leu	Val	Ile	Ala	Pro	Thr	Val	Leu	Leu	Thr	Met	Leu	Ser	Ser	Ala	20	25	30	
Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val	35	40	45	
Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser	50	55	60	
Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys	65	70	75	
Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu	80	85	90	
Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe	95	100	105	
Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg	110	115	120	
Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu	125	130	135	
Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser	140	145	150	
Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Leu	Ser	Leu	His	Leu	Arg	155	160	165	
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys	170	175	180	
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser	185	190	195	
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu				

200	205	210
His Leu Glu His	Asn Gln Phe Ser Lys	Leu Asn Leu Ala Leu Phe
215	220	225
Pro Arg Leu Val	Ser Leu Gln Asn Leu	Tyr Leu Gln Trp Asn Lys
230	235	240
Ile Ser Val Ile	Gly Gln Thr Met Ser	Trp Thr Trp Ser Ser Leu
245	250	255
Gln Arg Leu Asp	Leu Ser Gly Asn Glu	Ile Glu Ala Phe Ser Gly
260	265	270
Pro Ser Val Phe	Gln Cys Val Pro Asn	Leu Gln Arg Leu Asn Leu
275	280	285
Asp Ser Asn Lys	Leu Thr Phe Ile Gly	Gln Glu Ile Leu Asp Ser
290	295	300
Trp Ile Ser Leu	Asn Asp Ile Ser Leu	Ala Gly Asn Ile Trp Glu
305	310	315
Cys Ser Arg Asn	Ile Cys Ser Leu Val	Asn Trp Leu Lys Ser Phe
320	325	330
Lys Gly Leu Arg	Glu Asn Thr Ile Ile	Cys Ala Ser Pro Lys Glu
335	340	345
Leu Gln Gly Val	Asn Val Ile Asp Ala	Val Lys Asn Tyr Ser Ile
350	355	360
Cys Gly Lys Ser	Thr Thr Glu Arg Phe	Asp Leu Ala Arg Ala Leu
365	370	375
Pro Lys Pro Thr	Phe Lys Pro Lys Leu	Pro Arg Pro Lys His Glu
380	385	390
Ser Lys Pro Pro	Leu Pro Pro Thr Val	Gly Ala Thr Glu Pro Gly
395	400	405
Pro Glu Thr Asp	Ala Asp Ala Glu His	Ile Ser Phe His Lys Ile
410	415	420
Ile Ala Gly Ser	Val Ala Leu Phe Leu	Ser Val Leu Val Ile Leu
425	430	435
Leu Val Ile Tyr	Val Ser Trp Lys Arg	Tyr Pro Ala Ser Met Lys
440	445	450
Gln Leu Gln Gln	Arg Ser Leu Met Arg	Arg His Arg Lys Lys Lys
455	460	465
Arg Gln Ser Leu	Lys Gln Met Thr Pro	Ser Thr Gln Glu Phe Tyr
470	475	480
Val Asp Tyr Lys	Pro Thr Asn Thr Glu	Thr Ser Glu Met Leu Leu
485	490	495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
500 505 510

Cys Glu Val

<210> 386
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 386
ctgggatctg aacagtttcg gggc 24

<210> 387
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 387
ggtccccagg acatgggtctg tccc 24

<210> 388
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 388
gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
<211> 1449
<212> DNA
<213> Homo sapiens

<400> 389
agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
ttgactgtcc tttaaataatg tcaagatcca gacttttcag tgtcacctca 100
gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150
ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp	
				20					25					30	
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln	
			35						40					45	
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu	
			50						55					60	
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys	
			65						70					75	
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala	
			80						85					90	
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala	
			95						100					105	
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro	
			110						115					120	
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser	
			125						130					135	
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr					
			140						145						

<210> 391
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 391
 cttttcagtg tcacctcagc gatctc 26

<210> 392
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 392
 ccaaaacatg gagcaggaac agg 23

<210> 393
 <211> 47
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 393
ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 394
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aagctccgtg gcggcggcga cctgacgag aagcccacgg ccagctcagt 200
tctcttctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250
ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggatacaac 300
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gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450
tatgtcccag aaattgagtt tactgttgct tgtatttgga ctcatgtggg 500
gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550
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tctagcagag gaaaataaga acacagtggg tgtcgagaac ggtgcttcta 650
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attttgcaac gattggtgaa gctggagaac aaagttgact atattgttgt 750
gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttggtgc 800
cagtaaccac aaataaaaaga acgaatgtct cgggcagtat cagatagcag 850
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tgtacataaa aatttttaaag ttatttgttt gctttcaggc aagtctgttc 1050
aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggt 1100

Leu	Leu	Leu	Leu	Val	Phe	Gly	Leu	Ile	Trp	Gly	Leu	Met	Leu	Leu	20	25	30
His	Tyr	Thr	Phe	Gln	Gln	Pro	Arg	His	Gln	Ser	Ser	Val	Lys	Leu	35	40	45
Arg	Glu	Gln	Ile	Leu	Asp	Leu	Ser	Lys	Arg	Tyr	Val	Lys	Ala	Leu	50	55	60
Ala	Glu	Glu	Asn	Lys	Asn	Thr	Val	Asp	Val	Glu	Asn	Gly	Ala	Ser	65	70	75
Met	Ala	Gly	Tyr	Ala	Asp	Leu	Lys	Arg	Thr	Ile	Ala	Val	Leu	Leu	80	85	90
Asp	Asp	Ile	Leu	Gln	Arg	Leu	Val	Lys	Leu	Glu	Asn	Lys	Val	Asp	95	100	105
Tyr	Ile	Val	Val	Asn	Gly	Ser	Ala	Ala	Asn	Thr	Thr	Asn	Gly	Thr	110	115	120
Ser	Gly	Asn	Leu	Val	Pro	Val	Thr	Thr	Asn	Lys	Arg	Thr	Asn	Val	125	130	135
Ser	Gly	Ser	Ile	Arg											140		

<210> 396
 <211> 2639
 <212> DNA
 <213> Homo sapiens

<400> 396
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 accttcggcc ttttcgacag ctccagcctg actcgggtgg attgtagcgg 200
 cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250
 tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300
 gggccgggct acacgacgtt ggctggcctg gatctcagcc acaacctgct 350
 caccagcatc tcacccactg ctttctcccg ctttcgctac ctggagtcgc 400
 ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450
 agctcacccc tgagcgacgt gaaccttagc cacaaccagc tccgggaggt 500
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 acctctccca caacctcatt caccgcctcg tgccccaccc cacgagggcc 600
 ggootgctg cgcccacat tcagagcctg aacctggcct ggaaccggct 650

ccatgccgtg cccaacctcc gagacttgcc cctgcgctac ctgagcctgg 700
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 gccagtggc ttccgtgagc taccgggcct gcaggctctg gacctgtcgg 850
 gcaaccccaa gcttaactgg gcaggagctg aggtgttttc aggctgagc 900
 tcctgcagg agctggacct ttccggcacc aacctgggtgc ccctgcctga 950
 ggcgctgctc ctccacctcc cggcactgca gagcgtcagc gtgggccagg 1000
 atgtgcggtg ccggcgccctg gtgcgggagg gcacctaccc ccggaggcct 1050
 ggctccagcc ccaagggtgcc cctgcactgc gtagacaccc gggaatctgc 1100
 tgccaggggc cccaccatct tgtgacaaat ggtgtggccc agggccacat 1150
 aacagactgc tgtcctgggc tgcctcaggt cccgagtaac ttatgttcaa 1200
 tgtgccaaaca ccagtgggga gccgcaggc ctatgtggca gcgtcaccac 1250
 aggagtgtg ggcctaggag aggccttgga cctgggagcc acacctagga 1300
 gcaaagtctc acccctttgt ctacgttget tccccaaacc atgagcagag 1350
 ggacttcgat gccaaaccag actcgggtcc cctcctgctt cccttcccc 1400
 cttatcccc aagtgccttc cctcatgctt gggccggcct gacctgcaat 1450
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ccccacaggg cagtgaagtc tgtcttcccc cacctgccta gcccatcattc 2550
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<210> 397

<211> 353

<212> PRT

<213> Homo sapiens

<400> 397

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Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu	Val	Glu	Thr	20	25	30	
Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp	Cys	Ser	35	40	45	
Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp	Thr	50	55	60	
Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu	65	70	75	
Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu	Asp	80	85	90	
Leu	Ser	His	Asn	Leu	Leu	Thr	Ser	Ile	Ser	Pro	Thr	Ala	Phe	Ser	95	100	105	
Arg	Leu	Arg	Tyr	Leu	Glu	Ser	Leu	Asp	Leu	Ser	His	Asn	Gly	Leu	110	115	120	
Thr	Ala	Leu	Pro	Ala	Glu	Ser	Phe	Thr	Ser	Ser	Pro	Leu	Ser	Asp	125	130	135	
Val	Asn	Leu	Ser	His	Asn	Gln	Leu	Arg	Glu	Val	Ser	Val	Ser	Ala	140	145	150	

Phe	Thr	Thr	His	Ser	Gln	Gly	Arg	Ala	Leu	His	Val	Asp	Leu	Ser	155	160	165
His	Asn	Leu	Ile	His	Arg	Leu	Val	Pro	His	Pro	Thr	Arg	Ala	Gly	170	175	180
Leu	Pro	Ala	Pro	Thr	Ile	Gln	Ser	Leu	Asn	Leu	Ala	Trp	Asn	Arg	185	190	195
Leu	His	Ala	Val	Pro	Asn	Leu	Arg	Asp	Leu	Pro	Leu	Arg	Tyr	Leu	200	205	210
Ser	Leu	Asp	Gly	Asn	Pro	Leu	Ala	Val	Ile	Gly	Pro	Gly	Ala	Phe	215	220	225
Ala	Gly	Leu	Gly	Gly	Leu	Thr	His	Leu	Ser	Leu	Ala	Ser	Leu	Gln	230	235	240
Arg	Leu	Pro	Glu	Leu	Ala	Pro	Ser	Gly	Phe	Arg	Glu	Leu	Pro	Gly	245	250	255
Leu	Gln	Val	Leu	Asp	Leu	Ser	Gly	Asn	Pro	Lys	Leu	Asn	Trp	Ala	260	265	270
Gly	Ala	Glu	Val	Phe	Ser	Gly	Leu	Ser	Ser	Leu	Gln	Glu	Leu	Asp	275	280	285
Leu	Ser	Gly	Thr	Asn	Leu	Val	Pro	Leu	Pro	Glu	Ala	Leu	Leu	Leu	290	295	300
His	Leu	Pro	Ala	Leu	Gln	Ser	Val	Ser	Val	Gly	Gln	Asp	Val	Arg	305	310	315
Cys	Arg	Arg	Leu	Val	Arg	Glu	Gly	Thr	Tyr	Pro	Arg	Arg	Pro	Gly	320	325	330
Ser	Ser	Pro	Lys	Val	Pro	Leu	His	Cys	Val	Asp	Thr	Arg	Glu	Ser	335	340	345
Ala	Ala	Arg	Gly	Pro	Thr	Ile	Leu								350		

<210> 398

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 398

ccctgccagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caaccccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

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gtgggtctga ggggaccaga aggggtgagct acgttggtt tctggaagg 100
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atgtcattct ctatctattc actgcaagtg cctgctgttc caggccttac 200
ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250
cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300
ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350
tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400
ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450
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ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550
gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaatcga 600
tgctgcctcc tgcgccattt gctaagactc tatctggaca gggattttaa 650
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ccaattcctt tcttaccatc aagaaggacc tccggtcttc tcatgcccac 750

atgacatgcc attgtgggga ggaagcaatg aagaaataca gccagattct 800
 gagtcacttt gaaaagctgg aacctcaggc agcagttgtg aaggctttgg 850
 gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900
 agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950
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 cttgtgctgg tcacagtgtg tcttatttat gcattacttg cttccttgca 1050
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 atttttgtaa tatctttctg ctattggata tatttattag ttaatatt 1150
 tatttatttt ttgctattta atgtatttat ttttttactt ggacatgaaa 1200
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 gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400
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 ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
 aatcctacac ggccagcatg tattttctaca aataaagttt tctttgcata 1550
 ccaaaaaaaaa aaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

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Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
			20					25						30
Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
			35						40					45
Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu
			50						55					60
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu
			65						70					75
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser
			80						85					90

Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	95	100	105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	245	250	255
Trp	Met	Glu	Glu	Thr	Glu										260		

<210> 403
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-28
 <223> Synthetic construct.

<400> 403
 ctccctgtgggt ctccagattt caggccta 28

<210> 404
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 404
agtcctcctt agattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccgga ggaggaggag 50
aggcttttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggctaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
cctaggggac attgaagagg aaggctttct aaagctttgg caaggagtga 300
caccgcocat ttacagacac gtagtgtatt ctggaggtcg aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tcccccttgg aaatcagtca ttggagggat gatggctggt gttattggcc 450
agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa 500
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550
tgcatttgca aaaatccttag ctgaaggagg aatacgaggg ctttgggcag 600
gctgggtacc caatatacaa agagcagcac tggatgaatat gggagattta 650
accacttatg atacagtga acactacttg gtattgaata caccacttga 700
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgcttgatt caggctgttc aaggatgaagg attcatgagt ctatataaag 900
gctttttacc atcttggctg agaatgaccc cttgggtcaat ggtgttcttg 950
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
1 5 10 15

305

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Glu Met Ser Gly Val Ser Pro Phe
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<210> 407

<211> 31

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-31

<223> Synthetic construct.

<400> 407

cgcggtatccc gttatcgtct tgcgctactg c 31

<210> 408

<211> 34

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-34

<223> Synthetic construct.

<400> 408

gcggaattct taaaatggac tgactccact catc 34

<210> 409

<211> 1487

<212> DNA

<213> Homo sapiens

<400> 409

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 tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100
 cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150
 tagataattt tcgttgcca gaatgtgaat gtattgactg gaggtagaga 200
 agaaatgctg tggcatctgt tgcgcagggt atattgtttt ttacaggctg 250
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 ctgttttagga agaacagggt ctcgagtttg gcttttcatt ggtttcatgt 450
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 gttacccaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550

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<210> 410
 <211> 158
 <212> PRT
 <213> Homo sapiens

<400> 410
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 20 25 30
 Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala
 35 40 45
 Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr
 50 55 60
 Cys Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val
 65 70 75

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu
80 85 90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu
95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala
110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe
125 130 135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe
140 145 150

Gly Arg Thr Glu Glu Leu Trp Thr
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<210> 411

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 411

gtttgaggaa gctgggatac 20

<210> 412

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 412

ccaaactcga gcacctgttc 20

<210> 413

<211> 40

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-40

<223> Synthetic construct.

<400> 413

atggcaggct tctagataa ttttcgttgg ccagaatgtg 40

<210> 414

<211> 1337
<212> DNA
<213> Homo sapiens

<400> 414
gttgatggca aacttcctca aaggaggggc agagcctgcg cagggcagga 50
gcagctggcc cactggcggc ccgcaacact ccgtctcacc ctctggggccc 100
actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150
gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200
gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300
acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggccctcatc 350
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500
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ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700
gaaattcctt aaagaaattc cggggggtgc actggtgctg gtggcctcct 750
acgacgatcc agggaccaa atgaacgatg aaagcaggaa actcttctct 800
gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850
cttcatagga gccaaagacc tcaggggtaa aagccccttt gagcagttct 900
taaagaacag cccagacaca aacaaatacg agggatggcc agagctgctg 950
gagatggagg gctgcatgcc cccgaagcca ttttagggtg gctgtggctc 1000
ttcctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050
cccggcaggg gctgaggagg aggagcaggg ggtgctgctt ggaaggtgct 1100
gcaggtcctt gcaogctgtg tcgcgcctct cctcctcgga aacagaaccc 1150
tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200
accagctgtc tgtggagaga atggggtgct ttcgtcaggg actgctgacg 1250
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tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 415

Met	Arg	Val	Ser	Gly	Val	Leu	Arg	Leu	Leu	Ala	Leu	Ile	Phe	Ala	1	5	10	15
Ile	Val	Thr	Thr	Trp	Met	Phe	Ile	Arg	Ser	Tyr	Met	Ser	Phe	Ser	20	25	30	
Met	Lys	Thr	Ile	Arg	Leu	Pro	Arg	Trp	Leu	Ala	Ala	Ser	Pro	Thr	35	40	45	
Lys	Glu	Ile	Gln	Val	Lys	Lys	Tyr	Lys	Cys	Gly	Leu	Ile	Lys	Pro	50	55	60	
Cys	Pro	Ala	Asn	Tyr	Phe	Ala	Phe	Lys	Ile	Cys	Ser	Gly	Ala	Ala	65	70	75	
Asn	Val	Val	Gly	Pro	Thr	Met	Cys	Phe	Glu	Asp	Arg	Met	Ile	Met	80	85	90	
Ser	Pro	Val	Lys	Asn	Asn	Val	Gly	Arg	Gly	Leu	Asn	Ile	Ala	Leu	95	100	105	
Val	Asn	Gly	Thr	Thr	Gly	Ala	Val	Leu	Gly	Gln	Lys	Ala	Phe	Asp	110	115	120	
Met	Tyr	Ser	Gly	Asp	Val	Met	His	Leu	Val	Lys	Phe	Leu	Lys	Glu	125	130	135	
Ile	Pro	Gly	Gly	Ala	Leu	Val	Leu	Val	Ala	Ser	Tyr	Asp	Asp	Pro	140	145	150	
Gly	Thr	Lys	Met	Asn	Asp	Glu	Ser	Arg	Lys	Leu	Phe	Ser	Asp	Leu	155	160	165	
Gly	Ser	Ser	Tyr	Ala	Lys	Gln	Leu	Gly	Phe	Arg	Asp	Ser	Trp	Val	170	175	180	
Phe	Ile	Gly	Ala	Lys	Asp	Leu	Arg	Gly	Lys	Ser	Pro	Phe	Glu	Gln	185	190	195	
Phe	Leu	Lys	Asn	Ser	Pro	Asp	Thr	Asn	Lys	Tyr	Glu	Gly	Trp	Pro	200	205	210	
Glu	Leu	Leu	Glu	Met	Glu	Gly	Cys	Met	Pro	Pro	Lys	Pro	Phe		215	220		

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-21
<223> Synthetic construct.

<400> 416
gccatagtca cgacatggat g 21

<210> 417
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 417
ggatggccag agctgctg 18

<210> 418
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 418
aaagtacaag tgtggcctca tcaagc 26

<210> 419
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 419
tctgactcct aagtcaggca ggag 24

<210> 420
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 420
attctctcca cagacagctg gttc 24

<210> 421
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 421
gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100
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cacgccagga gtcgctcgc tctctctctc tctctctcac tctccctcc 200
ctctctctct gcctgtccta gtcctctagt cctcaaattc ccagtcacct 250
gcaccccttc ctgggacact atgttgttct ccgccctcct gctggagggtg 300
atctggatcc tggctgcaga tgggggtcaa cactggacgt atgaggggccc 350
acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500
ggacctgcac aacaatggcc acacagtgc actctctctg ccctctaccc 550
tgtatctggg tggacttccc cgaaaatatg tagctgcccc gctccacctg 600
cactgggggtc agaaaggatc cccagggggg tcagaacacc agatcaacag 650
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atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750
ggcatcctaa ttgagtgagg tgagactaag aatatagctt atgaacacat 800
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc 900
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tttccctaga tatactgcgg gatctctcct taggataaag agttgctgtt 1650
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t 1701

<210> 423

<211> 337

<212> PRT

<213> Homo sapiens

<400> 423

Met	Leu	Phe	Ser	Ala	Leu	Leu	Leu	Glu	Val	Ile	Trp	Ile	Leu	Ala
1				5				10					15	
Ala	Asp	Gly	Gly	Gln	His	Trp	Thr	Tyr	Glu	Gly	Pro	His	Gly	Gln
				20				25					30	
Asp	His	Trp	Pro	Ala	Ser	Tyr	Pro	Glu	Cys	Gly	Asn	Asn	Ala	Gln
				35				40					45	
Ser	Pro	Ile	Asp	Ile	Gln	Thr	Asp	Ser	Val	Thr	Phe	Asp	Pro	Asp
				50				55					60	
Leu	Pro	Ala	Leu	Gln	Pro	His	Gly	Tyr	Asp	Gln	Pro	Gly	Thr	Glu
				65				70					75	
Pro	Leu	Asp	Leu	His	Asn	Asn	Gly	His	Thr	Val	Gln	Leu	Ser	Leu

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Pro Ser Thr Leu Tyr Leu Gly Gly Leu Pro Arg Lys Tyr Val Ala
95 100 105

Ala Gln Leu His Leu His Trp Gly Gln Lys Gly Ser Pro Gly Gly
110 115 120

Ser Glu His Gln Ile Asn Ser Glu Ala Thr Phe Ala Glu Leu His
125 130 135

Ile Val His Tyr Asp Ser Asp Ser Tyr Asp Ser Leu Ser Glu Ala
140 145 150

Ala Glu Arg Pro Gln Gly Leu Ala Val Leu Gly Ile Leu Ile Glu
155 160 165

Val Gly Glu Thr Lys Asn Ile Ala Tyr Glu His Ile Leu Ser His
170 175 180

Leu His Glu Val Arg His Lys Asp Gln Lys Thr Ser Val Pro Pro
185 190 195

Phe Asn Leu Arg Glu Leu Leu Pro Lys Gln Leu Gly Gln Tyr Phe
200 205 210

Arg Tyr Asn Gly Ser Leu Thr Thr Pro Pro Cys Tyr Gln Ser Val
215 220 225

Leu Trp Thr Val Phe Tyr Arg Arg Ser Gln Ile Ser Met Glu Gln
230 235 240

Leu Glu Lys Leu Gln Gly Thr Leu Phe Ser Thr Glu Glu Glu Pro
245 250 255

Ser Lys Leu Leu Val Gln Asn Tyr Arg Ala Leu Gln Pro Leu Asn
260 265 270

Gln Arg Met Val Phe Ala Ser Phe Ile Gln Ala Gly Ser Ser Tyr
275 280 285

Thr Thr Gly Glu Met Leu Ser Leu Gly Val Gly Ile Leu Val Gly
290 295 300

Cys Leu Cys Leu Leu Leu Ala Val Tyr Phe Ile Ala Arg Lys Ile
305 310 315

Arg Lys Lys Arg Leu Glu Asn Arg Lys Ser Val Val Phe Thr Ser
320 325 330

Ala Gln Ala Thr Thr Glu Ala
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<210> 424

<211> 18

<212> DNA

<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 424
gtaaagtcgc tggccagc 18

<210> 425
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 425
cccgatctgc ctgctgta 18

<210> 426
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 426
ctgcactgta tggccattat tgtg 24

<210> 427
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 427
cagaaacca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

<400> 428
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gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn	
				80					85					90	
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr	
				95					100					105	
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro	
				110					115					120	
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly	
				125					130					135	
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp	
				140					145					150	
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln	
				155					160					165	
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp	
				170					175					180	
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His	
				185					190					195	
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln		
				200					205						

<210> 430
 <211> 1257
 <212> DNA
 <213> Homo Sapien

<400> 430
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 ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
 gccccgccgc ctccccgcag cggctccgcg gcctcctgct gctcctgctg 200
 ctgcagctgc ccgcgccgtc gagcgcctct gagatcccca aggggaagca 250
 aaaggcgcag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
 gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
 aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
 agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacacca 450
 actacaagca gtgttcatgg agttcattga attatggcat agatcttggg 500
 aaaattgcgg agtgtacatt tacaaagatg cgttcaaata gtgctctaag 550
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 agcgttggtta tttcacattc aatggagctg aatgttcagg acctcttccc 650

attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700
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acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150
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<210> 431

<211> 243

<212> PRT

<213> Homo Sapien

<400> 431

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly	1	5	10	15
Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala	20	25	30	
Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	35	40	45	
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	50	55	60	
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	65	70	75	
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	80	85	90	
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	95	100	105	
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	110	115	120	
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	125	130	135	

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
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